

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: November 3, 2005, 16:07:30 ; Search time 71 Seconds  
(without alignments)  
1378.174 Million cell updates/sec

Title: US-10-509-691-2  
Perfect score: 1363  
Sequence: 1 MPTSDSGEPRIAMKNGVT.....SGEYFAPDLSITTPGSLK 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1363	100.0	253	3	AAg27962 Arabidops
2	1363	100.0	253	6	ABP81243 Arabidops
3	1363	100.0	253	7	ADL63897 Thale cre
4	1296	95.1	240	3	AAg27963 Arabidops
5	651	47.8	225	7	ADD30096 Plant yle
6	651	47.8	225	7	ADD31439 Plant yle
7	651	47.8	225	8	ADL44297 Plant tra
8	402	29.5	209	3	AAg36752 Arabidops
9	402	29.5	209	7	ADD30372 Arabidops
10	402	29.5	209	8	ADL44299 Plant tra
11	402	29.5	226	3	AAg36751 Arabidops
12	377.5	27.7	193	3	AAg41702 Arabidops
13	377.5	27.7	194	3	AAg41701 Arabidops
14	377.5	27.7	204	3	AAg41700 Arabidops
15	377.5	27.7	204	7	ADD30374 Arabidops
16	377.5	27.7	204	8	ADL41899 Plant tra
17	368.5	27.0	208	3	AAg39024 Arabidops
18	368	27.0	176	3	AAg12100 Arabidops
19	368	27.0	198	3	AAg12099 Arabidops
20	320.5	23.5	299	3	AAg23893 Arabidops
21	320.5	23.5	299	3	AAg23892 Arabidops
22	320.5	23.5	307	3	AAg47820 Arabidops
23	320.5	23.5	307	7	ADD30376 Plant yle
24	320.5	23.5	307	8	ADL44303 Plant tra
25	320.5	23.5	307	8	ADL44303 Plant tra

26	320	23.5	372	7	ADD30208 Arabidops
27	320	23.5	372	8	ADL43855 Plant tra
28	318	23.3	194	8	ADN74777 Thale cre
29	317.5	23.3	399	7	ADD30362 Plant yle
30	317.5	23.3	399	8	ADL44285 Plant tra
31	317	23.3	352	7	ADJ11580 Rice prot
32	316.5	23.2	271	3	AAg23894 Arabidops
33	316.5	23.2	271	3	AAg47822 Arabidops
34	316.5	23.2	275	6	AAE30054 Arabidops
35	316.5	23.2	275	7	ADD31015 Arabidops
36	316.5	23.2	275	8	ADL44307 Plant tra
37	312	22.9	339	3	AAg44195 Arabidops
38	312	22.9	353	3	AAg44194 Arabidops
39	309	22.7	338	7	AAg53237 Arabidops
40	309	22.7	338	7	ADB31873 Arabidops
41	309	22.7	338	7	ADC46609 Thalecres
42	309	22.7	338	8	ADO02089 Thalecres
43	309	22.7	352	3	AAg53236 Arabidops
44	308.5	22.6	271	3	AAg20543 Arabidops
45	308.5	22.6	271	3	AAg28857 Arabidops

## ALIGNMENTS

RESULT 1	
ID	AAg27962 standard; protein; 253 AA.
XX	AAg27962;
AC	
XX	
DT	17-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana protein fragment SEQ ID NO: 33003.
XX	
KW	Protein identification; signal transduction pathway; metabolic pathway;
KW	hybridisation assay; genetic mapping; gene expression control; promoter;
KW	termination sequence.
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-00301439.
XX	
PR	25-FEB-1999; 99US-0121825P.
PR	05-MAR-1999; 99US-0123180P.
PR	09-MAR-1999; 99US-0123548P.
PR	23-MAR-1999; 99US-0125788P.
PR	25-MAR-1999; 99US-0126264P.
PR	29-MAR-1999; 99US-0126785P.
PR	01-APR-1999; 99US-0127462P.
PR	06-APR-1999; 99US-0128234P.
PR	08-APR-1999; 99US-0128714P.
PR	16-APR-1999; 99US-0129845P.
PR	19-APR-1999; 99US-0130077P.
PR	21-APR-1999; 99US-0130449P.
PR	23-APR-1999; 99US-0130510P.
PR	28-APR-1999; 99US-0130891P.
PR	30-APR-1999; 99US-0131449P.
PR	30-APR-1999; 99US-0132048P.
PR	30-APR-1999; 99US-0132407P.
PR	04-MAY-1999; 99US-0132484P.
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PR	06-MAY-1999; 99US-0132487P.
PR	07-MAY-1999; 99US-0132863P.
PR	11-MAY-1999; 99US-0134256P.
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PR 29-OCT-1999; 99US-0162142P.

Query Match 100.0%; Score 1363; DB 3; Length 253;  
Best Local Similarity 100.0%; Pred. No. 2,2e-104;  
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPTSDSGPRRIAMKPNVGVPIISDQEQQLPCPRCDSNTKFCYNNYNFSGPRHFCXAC 60  
DB 1 MPTSDSGPRRIAMKPNVGVPIISDQEQQLPCPRCDSNTKFCYNNYNFSGPRHFCXAC 60  
QY 61 RRYWTHGTLRDVPVGGGTRKSAKSRCTCSNSSSSVSGVNSNGVPLQTTPLVFPQSS 120  
DB 61 RRYWTHGTLRDVPVGGGTRKSAKSRCTCSNSSSSVSGVNSNGVPLQTTPLVFPQSS 120  
QY 121 ISNGVTHVTESDGGKSAISLCGFTSTLNNHNAATATHGSGSVYIGGFGIGLGSQFD 180  
DB 121 ISNGVTHVTESDGGKSAISLCGFTSTLNNHNAATATHGSGSVYIGGFGIGLGSQFD 180  
QY 181 DVSPGLGRAMPFSTVGTATTNNVSGNGHHAVPMPATWQFEGLESNAGGFGVSGEYPAW 240  
DB 181 DVSPGLGRAMPFSTVGTATTNNVSGNGHHAVPMPATWQFEGLESNAGGFGVSGEYPAW 240  
QY 241 PDLSTTTGNSLX 253  
DB 241 PDLSTTTGNSLX 253

RESULT 2  
ABP81243  
ID ABP81243 standard; protein; 253 AA.

XX AC ABP81243;  
XX DT 27-FEB-2003 (first entry)  
XX DE Arabidopsis thaliana protein #71 modulated by PTGS.  
XX KW Posttranscriptional gene silencing; PTGS; plant; transformation.  
XX OS Arabidopsis thaliana.  
XX PN WO200281695-A2.  
XX PD 17-OCT-2002.  
XX PF 05-APR-2002; 2002WO-EP003806.  
XX PR 06-APR-2001; 2001US-0282049P.  
XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.  
XX PA (FRIE-) FRIEDRICH MIESCHER INST.  
XX PI Zhu T, Glazov EA, Meins F, Wang X, Chang H;  
XX DR N-PSDB; AB242087.  
XX WPI; 2003-103337/09.

PT Novel polynucleic acid segment useful for modulating gene expression  
PT within a cell by posttranscriptional gene silencing, and for augmenting a  
PT plant cell genome.  
PS Claim 53; Page 301; 438pp; English.  
CC The invention relates to a novel isolated polynucleic acid segment  
CC modulated within a cell by posttranscriptional gene silencing (PTGS). The  
CC invention specifically relates to a method to identify an expression

CC product that is modulated by PTGS. The polynucleotide is useful for  
CC modulating the gene expression within a cell by PTGS, by introducing the  
CC polynucleic acid into a cell and expressing the nucleic acid segment in  
CC the cell to form a product. The polynucleic acid segment is also useful  
CC for augmenting a cell genome, and for augmenting a plant genome, by  
CC contacting a plant cell with the segment to produce a transformed plant  
CC cell, and growing the transformed plant cell to produce a differentiated  
CC transformed plant. The sequences shown in ABP81173 - ABP81298 represent  
CC the product of a segment of A. thaliana cDNA modulated by PTGS

Query Match 100.0%; Score 1363; DB 6; Length 253;

Best Local Similarity 100.0%; Pred. No. 2,2e-104;  
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPTSDSGPRRIAMKPNVGVPIISDQEQQLPCPRCDSNTKFCYNNYNFSGPRHFCXAC 60  
DB 1 MPTSDSGPRRIAMKPNVGVPIISDQEQQLPCPRCDSNTKFCYNNYNFSGPRHFCXAC 60  
QY 61 RRYWTHGTLRDVPVGGGTRKSAKSRCTCSNSSSSVSGVNSNGVPLQTTPLVFPQSS 120  
DB 61 RRYWTHGTLRDVPVGGGTRKSAKSRCTCSNSSSSVSGVNSNGVPLQTTPLVFPQSS 120  
QY 121 ISNGVTHVTESDGGKSAISLCGFTSTLNNHNAATATHGSGSVYIGGFGIGLGSQFD 180  
DB 121 ISNGVTHVTESDGGKSAISLCGFTSTLNNHNAATATHGSGSVYIGGFGIGLGSQFD 180  
QY 181 DVSPGLGRAMPFSTVGTATTNNVSGNGHHAVPMPATWQFEGLESNAGGFGVSGEYPAW 240  
DB 181 DVSPGLGRAMPFSTVGTATTNNVSGNGHHAVPMPATWQFEGLESNAGGFGVSGEYPAW 240  
QY 241 PDLSTTTGNSLX 253  
DB 241 PDLSTTTGNSLX 253

RESULT 3  
ADL63897  
ID ADL63897 standard; protein; 253 AA.

XX AC ADL63897;  
XX DT 20-MAY-2004 (first entry)  
XX DE Thale cress drought tolerance 2 (DRO2) protein Segd 2.  
XX KW Transgenic; plant; drought tolerance 2; DRO2; abiotic stress;  
XX KW salt stress; freezing; protectant; agricultural crop; thale cress.  
XX OS Arabidopsis thaliana.  
XX PN WO2003081988-A2.  
XX PD 09-OCT-2003.  
XX PF 27-MAR-2003; 2003WO-US009479.  
XX PR 27-MAR-2002; 2002US-0368650P.  
XX PA (AGRI-) AGRINOMICS LLC.  
XX PI Van Winkle J, Liu XL, Fitch JR, Shulaev V;  
XX DR N-PSDB; ADL63896.  
XX WPI; 2003-812489/76.

PT New transgenic plants comprising the drought tolerant 2 (DRO2) gene and  
PT having increased tolerance to drought, useful in generating crops and/or  
PT other plant species having improved ability to survive in low water  
PT conditions.  
PS Claim 1; SEQ ID NO 2; 23pp; English.

XX This invention relates to generating novel transgenic plants with an  
CC improved drought tolerance phenotype. Specifically, it relates to plants  
CC transfected with a vector containing a heterologous drought tolerant 2  
CC (DRO2) gene. The present invention describes the development of  
CC genetically modified plants that overexpress the DRO2 gene, such that the  
CC overall health of the transgenic plant is improved compared to controls  
CC and in particular it displays increased tolerance to other abiotic  
CC stresses including salt stress and freezing. Accordingly, such  
CC compositions are plant protectants and hence are useful for the  
CC generation of agricultural crops such as cotton, wheat, corn and beans  
CC that exhibit an improved ability to survive in low water conditions. This  
CC polypeptide sequence is the thale cress DRO2 protein sequence of the  
CC invention.

XX Sequence 253 AA;

Query Match 100.0%; Score 1363; DB 7; Length 253;  
Best Local Similarity 100.0%; Pred. No. 2.2e-104;  
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPTSDSGPRRIAMKPNQVTPISDQEQLPKPCDSSNTKFCYNNYNFQPHFKAC 60  
Db 1 MPTSDSGPRRIAMKPNQVTPISDQEQLPKPCDSSNTKFCYNNYNFQPHFKAC 60  
QY 61 RRYWTHGGTLRDVPGGTRKSAKRSRTCSNSSSSVSGVSNNGVPLQTPVLPFQSS 120  
Db 61 RRYWTHGGTLRDVPGGTRKSAKRSRTCSNSSSSVSGVSNNGVPLQTPVLPFQSS 120  
QY 121 ISNGVTHVTESDQKGSALICGSFTSTLLNHNAAATHTHSGSVIGIGGFGIGSGFD 180  
Db 121 ISNGVTHVTESDQKGSALICGSFTSTLLNHNAAATHTHSGSVIGIGGFGIGSGFD 180  
QY 181 DVSFGLGRAMPFSTVGATTTNGSNGGHAVMPATWQEGLESNAGGFGVSGEYPAW 240  
Db 181 DVSFGLGRAMPFSTVGATTTNGSNGGHAVMPATWQEGLESNAGGFGVSGEYPAW 240  
QY 241 PDLSTTPGNSLK 253  
Db 241 PDLSTTPGNSLK 253

RESULT 4  
AAG27963  
ID AAG27963 standard; protein; 240 AA.  
XX  
AC AAG27963;  
XX  
DT 17-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 33004.  
XX  
KM Protein identification; signal transduction pathway; metabolic pathway;  
KM hybridisation assay; genetic mapping; gene expression control; promoter;  
KM termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-00301439.  
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PR 25-FEB-1999; 99US-0121825P.  
PR 05-MAR-1999; 99US-0123180P.  
PR 09-MAR-1999; 99US-0123548P.  
PR 23-MAR-1999; 99US-0125788P.  
PR 25-MAR-1999; 99US-0126264P.  
PR 29-MAR-1999; 99US-0126785P.  
PR 01-APR-1999; 99US-0127462P.  
PR 06-APR-1999; 99US-0128234P.  
PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.  
PR 19-APR-1999; 99US-0130047P.  
PR 21-APR-1999; 99US-0130449P.  
PR 23-APR-1999; 99US-0130510P.  
PR 23-APR-1999; 99US-0130891P.  
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PR 30-APR-1999; 99US-0132048P.  
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PR 11-MAY-1999; 99US-0134256P.  
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PR 10-JUN-1999; 99US-0138847P.  
PR 14-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
PR 16-JUN-1999; 99US-0139453P.  
PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
PR 23-JUN-1999; 99US-0140354P.  
PR 24-JUN-1999; 99US-0140695P.  
PR 28-JUN-1999; 99US-0140823P.  
PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
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PR 19-JUL-1999; 99US-0144331P.  
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PR 19-JUL-1999; 99US-0144333P.

PR 19-JUL-1999; 99US-0144334P.  
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PR 20-JUL-1999; 99US-0144884P.  
PR 21-JUL-1999; 99US-0144814P.  
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PR 09-AUG-1999; 99US-0147416P.  
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PR 18-AUG-1999; 99US-0149426P.  
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PR 30-AUG-1999; 99US-0151303P.  
PR 31-AUG-1999; 99US-0151438P.  
PR 01-SEP-1999; 99US-0151930P.  
PR 07-SEP-1999; 99US-0152363P.  
PR 10-SEP-1999; 99US-0153708P.  
PR 13-SEP-1999; 99US-0153758P.  
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PR 04-OCT-1999; 99US-0157117P.  
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PR 06-OCT-1999; 99US-0157865P.  
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PR 14-OCT-1999; 99US-0159329P.  
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PR 14-OCT-1999; 99US-0159637P.  
PR 18-OCT-1999; 99US-0159638P.  
PR 18-OCT-1999; 99US-0159584P.  
PR 21-OCT-1999; 99US-0160741P.  
PR 21-OCT-1999; 99US-0160767P.  
PR 21-OCT-1999; 99US-0160768P.  
PR 21-OCT-1999; 99US-0160770P.  
PR 21-OCT-1999; 99US-0160814P.  
PR 21-OCT-1999; 99US-0160815P.  
PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
PR 22-OCT-1999; 99US-0160989P.  
PR 25-OCT-1999; 99US-0161404P.  
PR 25-OCT-1999; 99US-0161405P.  
PR 25-OCT-1999; 99US-0161406P.  
PR 26-OCT-1999; 99US-0161359P.  
PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
PR 28-OCT-1999; 99US-0161920P.  
PR 28-OCT-1999; 99US-0161922P.  
PR 28-OCT-1999; 99US-0161932P.  
PR 29-OCT-1999; 99US-0162142P.

Query Match 95.1%; Score 1296; DB 3; Length 240;  
Best Local Similarity 100.0%; Pred. No. 7e-99;  
Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 MKPNGVTVPISDQOLPCPRCDSSNTKFCYNNYNNFQOPRHFCACRRYTHGTLRDV 73  
DB 1 MKPNGVTVPISDQOLPCPRCDSSNTKFCYNNYNNFQOPRHFCACRRYTHGTLRDV 60  
QY 74 PVGGTRRSARSRSCSSSSSVSGVVSNSNGVPLQTTPVLPFPOSSISNGVHTVTESD 133  
DB 61 PVGGTRRSARSRSCSSSSSVSGVVSNSNGVPLQTTPVLPFPOSSISNGVHTVTESD 120  
QY 134 GKGSALSLCGSFSTLLNHNAAATATHGSGSVIGIGFSGIGSGFDDVSFELGRAMMPE 193  
DB 121 GKGSALSLCGSFSTLLNHNAAATATHGSGSVIGIGFSGIGSGFDDVSFELGRAMMPE 180  
QY 194 STVGATTTTNGSNGGHHAVMPATWQFGLSESNAGGFVSGEYFAMPDLSTTPGNSLX 253  
DB 191 STVGATTTTNGSNGGHHAVMPATWQFGLSESNAGGFVSGEYFAMPDLSTTPGNSLX 240

RESULT 5  
ADD30096 standard; protein; 225 AA.  
XX ID ADD30096  
XX AC ADD30096;  
XX DT 15-JAN-2004 (first entry)  
XX DE Plant yield-related protein from clone G1897.  
XX KW transcription factor; transgenic plant; growth rate; senescence;  
XX KW seed germination rate; plant vigor; seedling vigor.  
OS Arabidopsis thaliana.  
XX PN W02003013227-A2.  
XX PD 20-FEB-2003.  
XX PF 09-AUG-2002; 2002WO-US025805.  
XX PR 09-AUG-2001; 2001US-0310847P.  
XX PR 19-NOV-2001; 2001US-0336049P.  
XX PR 11-DEC-2001; 2001US-0336922P.  
XX PR 14-JUN-2002; 2002US-00171468.

PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
 XX  
 PI Ratcliffe O, Riechmann JL, Adam LJ, Dubell AT, Heard JE;  
 PI Pilgrim ML, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu G;  
 PI Brown PE;  
 XX  
 DR WPI: 2003-248221/24.  
 DR N-PSDB; ADD30095.  
 XX  
 PT New plant transcription factor polynucleotides and polypeptides, useful  
 PT in producing transgenic plants with commercially valuable properties,  
 PT such as an alteration in a plant growth characteristic, e.g. growth rate  
 PT or apomixis.  
 XX  
 PS Disclosure; SEQ ID NO 125; 454bp; English.  
 XX  
 CC The invention relates to a number of isolated Arabidopsis thaliana cDNA  
 CC sequences and their encoded proteins which are especially transcription  
 CC factor related cDNA's and proteins. The isolated or recombinant plant  
 CC transcription factor polynucleotides and polypeptides are useful in  
 CC producing transgenic plants with commercially valuable properties, i.e.  
 CC modified or altered desirable traits as compared to a reference plant,  
 CC such as an alteration in a plant growth characteristic, e.g. growth rate,  
 CC germination rate of seeds, vigor of plants and seedlings, or leaf and  
 CC flower senescence. Sequence information related to the polynucleotides  
 CC and polypeptides can also be used in bioinformatic search methods. The  
 CC transgenic plant is useful for growing a progeny plant from a parent  
 CC plant. This sequence represents one of the proteins of the invention.  
 CC  
 XX  
 SQ Sequence 225 AA;  
 Query Match 47.8%; Score 651; DB 7; Length 225;  
 Best Local Similarity 55.5%; Pred. No. 1.4e-45;  
 Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;  
 QY 1 MPTDSGEPRIAMKPNQ---VTVPISDQEQLPCCPCDSSNTKFCYNNYNNFSQPRHF 56  
 DB 1 MP-SEFSBSRRVPKIPHGGGSAIP-TDQEQOLSCPCSESTNTKFCYNNYNNFSQPRHF 58  
 QY 57 CKAARRYTHGGTLRDVPGGTRKSAKRSRTCSNSSSSVGVNSNGVPLQTTPLVF 116  
 DB 59 CKSCRRTWTHGGTLRDIPVGGVSRKSKRSRTYSSAATTSVVG---SRNFPLOATPLVF 114  
 QY 117 POSSISNGVTHVTESDQKGSALSLGCSFTSTLLNNAATAATATGSGSVIGIGFGIGLG 176  
 DB 115 POSSSNGGIT-----TAKGSASSFYGGF-SSLINYNAAVSRNGPGGFGNPDAPFGIGLG 167  
 QY 177 SG--FDVVSFGLGRAMPFSTVGT--ATTNVSNGGHHAVMPATWQFEGLESNAGGCF 232  
 DB 168 HGSYVEDVRYGQGITWPFSSGATDAATTS-----HIAQIPATWQFEGQESKV--GF 218  
 QY 233 VSGEYFA 239  
 DB 219 VSGDYVA 225  
 RESULT 6  
 ADE31439 ID ADE31439 standard; protein; 225 AA.  
 AC ADE31439;  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Plant yield related protein from clone G1897.  
 XX  
 KM transcription factor; transgenic plant; salt stress resistance;  
 KM osmotic stress resistance; freezing tolerance; drought tolerance;  
 KM low humidity tolerance; radiation resistance.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN WO2003013228-A2.

XX  
 PD 20-FEB-2003.  
 XX  
 PF 09-AUG-2002; 2002MO-US025808.  
 XX  
 PF 09-AUG-2001; 2001US-0310847P.  
 XX  
 PR 19-NOV-2001; 2001US-0336049P.  
 PR 11-DEC-2001; 2001US-0338692P.  
 PR 14-JUN-2002; 2002US-00171468.  
 XX  
 PA (MEND-) MENDEL BIOTECHNOLOGY INC.  
 XX  
 PI Heard JE, Riechmann JL, Creelman RA, Keddie J, Pilgrim ML;  
 PI Dubell AN, Jiang C, Ratcliffe O, Pineda O, Yu G, Brown PE;  
 PI Brown PE;  
 XX  
 DR WPI: 2003-248222/24.  
 DR N-PSDB; ADE31438.  
 XX  
 PT New plant transcription factor polynucleotides and polypeptides, useful  
 PT in producing transgenic plants with commercially valuable properties,  
 PT i.e. modified desirable traits, e.g. salt stress resistance or tolerance  
 PT to freezing.  
 XX  
 PS Disclosure; SEQ ID NO 6; 311bp; English.  
 XX  
 CC The invention relates to a number of isolated cDNA sequences and their  
 CC encoded proteins which are especially transcription factor related cDNA's  
 CC and proteins. The isolated or recombinant plant transcription factor  
 CC polynucleotides and polypeptides are useful in producing transgenic  
 CC plants with commercially valuable properties, i.e. modified or altered  
 CC desirable traits as compared to a reference plant, e.g. salt stress  
 CC resistance, osmotic stress resistance, tolerance to freezing, drought,  
 CC low humidity tolerance, or radiation resistance. Sequence information  
 CC related to the polynucleotides and polypeptides can also be used in  
 CC bioinformatic search methods. The transgenic plant is useful for growing  
 CC a progeny plant from a parent plant. This sequence represents one of the  
 CC proteins of the invention.  
 CC  
 XX  
 SQ Sequence 225 AA;  
 Query Match 47.8%; Score 651; DB 7; Length 225;  
 Best Local Similarity 55.5%; Pred. No. 1.4e-45;  
 Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;  
 QY 1 MPTDSGEPRIAMKPNQ---VTVPISDQEQLPCCPCDSSNTKFCYNNYNNFSQPRHF 56  
 DB 1 MP-SEFSBSRRVPKIPHGGGSAIP-TDQEQOLSCPCSESTNTKFCYNNYNNFSQPRHF 58  
 QY 57 CKAARRYTHGGTLRDVPGGTRKSAKRSRTCSNSSSSVGVNSNGVPLQTTPLVF 116  
 DB 59 CKSCRRTWTHGGTLRDIPVGGVSRKSKRSRTYSSAATTSVVG---SRNFPLOATPLVF 114  
 QY 117 POSSISNGVTHVTESDQKGSALSLGCSFTSTLLNNAATAATATGSGSVIGIGFGIGLG 176  
 DB 115 POSSSNGGIT-----TAKGSASSFYGGF-SSLINYNAAVSRNGPGGFGNPDAPFGIGLG 167  
 QY 177 SG--FDVVSFGLGRAMPFSTVGT--ATTNVSNGGHHAVMPATWQFEGLESNAGGCF 232  
 DB 168 HGSYVEDVRYGQGITWPFSSGATDAATTS-----HIAQIPATWQFEGQESKV--GF 218  
 QY 233 VSGEYFA 239  
 DB 219 VSGDYVA 225  
 RESULT 7  
 ADI44297 ID ADI44297 standard; protein; 225 AA.  
 AC ADI44297;  
 XX  
 DT 22-APR-2004 (first entry)  
 XX

DE Plant transcription factor related polypeptide #1737.  
 XX transgenic; plant; enhanced tolerance to abiotic stress;  
 KW glyophosphate tolerance; hormone sensitivity; disease resistance;  
 KW sugar sensing; flowering; flower structure; stem bifurcation;  
 KW branching pattern; apical dominance; trichome; stem morphology;  
 KW root growth; root hair; seed development; cell proliferation;  
 KW cell differentiation; premature senescence; necrosis; plant size;  
 KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;  
 KW plant anthocyanin; light response; shade avoidance; bioinformatic;  
 KW transcription factor; db.  
 XX  
 XX Unidentified.  
 OS  
 XX US2004019927-A1.  
 PN  
 XX 29-JAN-2004.  
 PD  
 XX 25-FEB-2003; 2003US-00374780.  
 PF  
 XX 18-APR-2001; 2001US-00837944.  
 PR  
 XX (SHER/) SHERMAN B K.  
 PA (RIEC/) RIECHMANN J L.  
 PA (JIANG/) JIANG C.  
 PA (HEAR/) HEARD J E.  
 PA (HAAK/) HAAKE V.  
 PA (CREE/) CREELMAN R A.  
 PA (RATC/) RATCLIFFE O.  
 PA (ADAM/) ADAM L J.  
 PA (REUB/) REUBER T L.  
 PA (KEDD/) KEDDIE J.  
 PA (BROU/) BROUN P E.  
 PA (PIUG/) PILGRIM M L.  
 PA (DUBE/) DUBBEL A N.  
 PA (PINE/) PINEDA O.  
 PA (YUGG/) YU G.  
 XX  
 PI Sherman BK, Riechmann JL, Jiang C, Heard JE, Haake V;  
 PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE;  
 PI Pilgrim ML, Dubell AN, Pineda O, Yu G;  
 DR WP1; 2004-132245/13.  
 DR N-PSDB; ADI44296.  
 XX  
 PT New transgenic plant comprising a recombinant polynucleotide of any one  
 PT of more than 500 nucleotide sequences, useful in bioinformatic search  
 PT methods.  
 PS  
 XX Disclosure; SEQ ID NO 2760; 435bp; English.  
 CC The invention describes a transgenic plant comprising a recombinant  
 CC polynucleotide of any one of more than 500 nucleotide sequences fully  
 CC defined in the specification or its complement. The method of the  
 CC invention can be used to produce a plant having altered traits such as:  
 CC enhanced tolerance to abiotic stress; glyophosphate tolerance; hormone  
 CC sensitivity; disease resistance; sugar sensing; early or late flowering;  
 CC altered flower structure, change in stem bifurcations; altered branching  
 CC pattern; reduced apical dominance; reduced trichome density; lack of  
 CC trichomes; reduced ectopic trichome development; altered morphology;  
 CC development; increase in trichome number; altered stem morphology;  
 CC increased root growth; increased root hairs; altered seed development;  
 CC altered cell proliferation or cell differentiation; rapid development;  
 CC premature senescence; increased necrosis; increase in seedling or plant  
 CC size; decreased plant size; leaf morphology; increase in seedling or plant  
 CC biochemistry; increase in root anthocyanins; increase in plant  
 CC anthocyanins, or alteration in light response or shade avoidance. The  
 CC transgenic plant, polynucleotides and polypeptides are useful in  
 CC bioinformatic search methods. This sequence represents a plant  
 CC transcription factor related polynucleotide.  
 CC  
 XX Sequence 225 AA;  
 SQ

Query Match 47.8%; Score 651; DB 8; Length 225;  
 Best Local Similarity 55.5%; Pred. No. 1.4e-45;  
 Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;  
 QY 1 MPTSDSGEPRRIAMKPNQ---VTVPIDQOEQLPCPRCDSNTYFCYNNNTFSQPRHF 56  
 DB 1 MP-SFSSRSRRPDKPHQCGGSAIIP-IDQEQQLCPCPCESNTYFCYNNNTFSQPRHF 58  
 QY 57 CKACRRYTHGCTADVPVGGGTRSAKRSRRCSSSSSSSVSGVNSNGVLOTTPVLF 116  
 DB 59 CKSCRRYTHGCTADVPVGGGTRSAKRSRRCSSSSSSSVSGVNSNGVLOTTPVLF 114  
 QY 117 POSSISNGVTHTVTESDQGSALSLGSGFTSTLNNNAATATHGSGSVIGIGFGIG 176  
 DB 115 POSSSNGGIT-----TAKGSASSFYGGF-SGLIYNNAASVNGGCGGNGPDAFGLGIG 167  
 QY 177 SG-FDDVSPGLGRAMPFSTVGT--ATTNVGNGGHHAVMPATWQFEGLESNAGGF 232  
 DB 168 HGSYYEDVRYGCGITVWPFPSSGATDAATTTS-----HIAQIPATWQFEGGSHV--GF 218  
 QY 233 VSGEYFA 239  
 DB 219 VSGDYVA 225  
 RESULT 8  
 ID AAG36752 standard; protein, 209 AA.  
 XX AAG36752;  
 AC  
 XX 18-OCT-2000 (first entry)  
 DT  
 XX Arabidopsis thaliana protein fragment SEQ ID NO: 45085.  
 DE  
 XX Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
 KW  
 OS Arabidopsis thaliana.  
 PN EP1033405-A2.  
 XX  
 XX 06-SEP-2000.  
 PD  
 XX  
 XX 25-FEB-2000; 2000EP-00301439.  
 PF  
 XX 25-FEB-1999; 99US-0121825P.  
 PR 05-MAR-1999; 99US-0123180P.  
 PR 09-MAR-1999; 99US-0123548P.  
 PR 23-MAR-1999; 99US-0125788P.  
 PR 25-MAR-1999; 99US-0126264P.  
 PR 29-MAR-1999; 99US-0126785P.  
 PR 01-APR-1999; 99US-0127462P.  
 PR 06-APR-1999; 99US-0128234P.  
 PR 08-APR-1999; 99US-0128714P.  
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 PR 14-MAY-1999; 99US-0134221P.

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PR 03-JUN-1999; 99US-0137528P.  
PR 04-JUN-1999; 99US-0137502P.  
PR 07-JUN-1999; 99US-0137724P.  
PR 08-JUN-1999; 99US-0138094P.  
PR 10-JUN-1999; 99US-0138540P.  
PR 14-JUN-1999; 99US-0138847P.  
PR 16-JUN-1999; 99US-0139119P.  
PR 16-JUN-1999; 99US-0139452P.  
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PR 17-JUN-1999; 99US-0139492P.  
PR 18-JUN-1999; 99US-0139454P.  
PR 18-JUN-1999; 99US-0139455P.  
PR 18-JUN-1999; 99US-0139456P.  
PR 18-JUN-1999; 99US-0139457P.  
PR 18-JUN-1999; 99US-0139458P.  
PR 18-JUN-1999; 99US-0139459P.  
PR 18-JUN-1999; 99US-0139460P.  
PR 18-JUN-1999; 99US-0139461P.  
PR 18-JUN-1999; 99US-0139462P.  
PR 18-JUN-1999; 99US-0139463P.  
PR 18-JUN-1999; 99US-0139750P.  
PR 18-JUN-1999; 99US-0139763P.  
PR 21-JUN-1999; 99US-0139817P.  
PR 22-JUN-1999; 99US-0139899P.  
PR 23-JUN-1999; 99US-0140353P.  
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PR 24-JUN-1999; 99US-0140695P.  
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PR 29-JUN-1999; 99US-0140991P.  
PR 30-JUN-1999; 99US-0141287P.  
PR 01-JUL-1999; 99US-0141842P.  
PR 01-JUL-1999; 99US-0142154P.  
PR 02-JUL-1999; 99US-0142055P.  
PR 06-JUL-1999; 99US-0142390P.  
PR 08-JUL-1999; 99US-0142803P.  
PR 09-JUL-1999; 99US-0142920P.  
PR 12-JUL-1999; 99US-0142977P.  
PR 13-JUL-1999; 99US-0143542P.  
PR 14-JUL-1999; 99US-0143624P.  
PR 15-JUL-1999; 99US-0144005P.  
PR 16-JUL-1999; 99US-0144085P.  
PR 16-JUL-1999; 99US-0144086P.  
PR 19-JUL-1999; 99US-0144325P.  
PR 19-JUL-1999; 99US-0144331P.  
PR 19-JUL-1999; 99US-0144332P.  
PR 19-JUL-1999; 99US-0144333P.  
PR 19-JUL-1999; 99US-0144334P.  
PR 19-JUL-1999; 99US-0144335P.  
PR 20-JUL-1999; 99US-0144352P.  
PR 20-JUL-1999; 99US-0144632P.  
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PR 25-OCT-1999; 99US-0161405P.



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PR 28-OCT-1999; 99US-0161932P.
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PR 29-OCT-1999; 99US-0162142P.

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Best Local Similarity 39.0%; Pred. No. 4.8e-25;
Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;

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DB 1 MP-SEPNQTRPTRVQPSFAAYPPVLAEPPLPCPRCNSITTKFCYNNYNNLAQPRYCKSC 59

QY 61 RRYWTHGGLTLDVPPVGGTRK-SAKRSRTCSN--SSSSVSGVYNSNGVPLQTPVLP 117
DB 60 RRYWTHGGLTLDVPPVGGTRSSSRHRSFSTTATSSSSSVITTTQEPATTEA---S 116

QY 118 QSSISNGVTHVTESDGGKGSALSLCGSFTSTLLNHNAAATATHSGSVIGIG--FGIGL 175
DB 117 QTKYTNLIS-----GHGSPASLIGL-----GSGN---GGLDYGRGY 149

QY 176 GSGFDVVSFG-LGRAMPFSTVGTATTNNVSGNGGHAVPMPATWQFGLSNNAGGFSVS 234
DB 150 GYGLEEMSIGYLGD-----SSVGEIPV--VDCCGD-----TWQIGEIRKSG----- 190

QY 235 GEYFAMPDLSTITPNSLX 253
DB 191 GDSLWPGLEISMOTNDVK 209

RESULT 9
ADD30372
ID ADD30372 standard; proein; 209 AA.
XX
AC ADD30372;
XX
DT 15-JAN-2004 (first entry)
XX
DE Plant yield-related protein from clone G1898.
XX
KW transcription factor; transgenic plant; growth rate; senescence;
XX seed germination rate; plant vigor; seedling vigor.
XX
OS Arabidopsis thaliana.
XX
PN WO2003013227-A2.
XX
PD 20-FEB-2003.
XX
PF 09-AUG-2002; 2002WO-US025805.
XX
PR 09-AUG-2001; 2001US-0310847P.
PR 19-NOV-2001; 2001US-0336049P.
PR 11-DEC-2001; 2001US-0336922P.
PR 14-JUN-2002; 2002US-00171468.
XX
PA (MEND-) MENDEL BIOTECHNOLOGY INC.
XX
PI Ratcliffe O, Riechmann JL, Adam LJ, Dubell AT, Heard JB;
PI Pilgrim WL, Jiang C, Reuber TL, Creelman RA, Pineda O, Yu G;
PI Brown PE;
XX
XX MPI; 2003-248221/24.
XX
XX N-PSDB; ADD30371.
XX
XX New plant transcription factor polynucleotides and polypeptides, useful
XX in producing transgenic plants with commercially valuable properties,
XX PT such as an alteration in a plant growth characteristic, e.g. growth rate
XX or apomixis.

```

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XX
PS Disclosure; SEQ ID NO 401; 454bp; English.
XX
CC The invention relates to a number of isolated Arabidopsis thaliana cDNA
CC sequences and their encoded proteins which are especially transcription
CC factor related cDNA's and proteins. The isolated or recombinant plant
CC transcription factor polynucleotides and polypeptides are useful in
CC producing transgenic plants with commercially valuable properties, i.e.
CC modified or altered desirable traits as compared to a reference plant,
CC such as an alteration in a plant growth characteristic, e.g. growth rate,
CC germination rate of seeds, vigor of plants and seedlings, or leaf and
CC flower senescence. Sequence information related to the polynucleotides
CC and polypeptides can also be used in bioinformatic search methods. The
CC transgenic plant is useful for growing a progeny plant from a parent
CC plant. This sequence represents one of the proteins of the invention.
XX
SQ Sequence 209 AA;

Query Match 29.5%; Score 402; DB 7; Length 209;
Best Local Similarity 39.0%; Pred. No. 4.8e-25;
Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;

QY 1 MPTSDSGPRRIAMKPNKNGVTVPISDQEQOLPCPRCDSNTKFCYNNYNNFSQPRHFCAC 60
DB 1 MP-SEPNQTRPTRVQPSFAAYPPVLAEPPLPCPRCNSITTKFCYNNYNNLAQPRYCKSC 59

QY 61 RRYWTHGGLTLDVPPVGGTRK-SAKRSRTCSN--SSSSVSGVYNSNGVPLQTPVLP 117
DB 60 RRYWTHGGLTLDVPPVGGTRSSSRHRSFSTTATSSSSSVITTTQEPATTEA---S 116

QY 118 QSSISNGVTHVTESDGGKGSALSLCGSFTSTLLNHNAAATATHSGSVIGIG--FGIGL 175
DB 117 QTKYTNLIS-----GHGSPASLIGL-----GSGN---GGLDYGRGY 149

QY 176 GSGFDVVSFG-LGRAMPFSTVGTATTNNVSGNGGHAVPMPATWQFGLSNNAGGFSVS 234
DB 150 GYGLEEMSIGYLGD-----SSVGEIPV--VDCCGD-----TWQIGEIRKSG----- 190

QY 235 GEYFAMPDLSTITPNSLX 253
DB 191 GDSLWPGLEISMOTNDVK 209

RESULT 10
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ID ADI44299 standard; proein; 209 AA.
XX
AC ADI44299;
XX
DT 22-APR-2004 (first entry)
XX
DE Plant transcription factor related polypeptide #1738.
XX
KW transgenic; plant; enhanced tolerance to abiotic stress;
KW glyophosphate tolerance; hormone sensitivity; disease resistance;
KW sugar sensing; flowering; flower structure; stem bifurcation;
KW branching pattern; apical dominance; trichome; stem morphology;
KW root growth; root hair; seed development; cell proliferation;
KW cell differentiation; premature senescence; necrosis; plant size;
KW leaf morphology; seed morphology; seed biochemistry; root anthocyanin;
KW plant anthocyanin; light response; shade avoidance; bioinformatic;
KW transcription factor; db.
XX
OS Unidentified.
XX
PN US2004019927-A1.
XX
PD 29-JAN-2004.
XX
PF 25-FEB-2003; 2003US-00374780.
XX
XX 18-APR-2001; 2001US-00837944.
XX

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PA (SHER/) SHERMAN B K.  
PA (RIEC/) RIECHMANN J L.  
PA (JIANG/) JIANG C.  
PA (HEAR/) HEARD J E.  
PA (HAK/) HAKE V.  
PA (CREE/) CREELMAN R A.  
PA (RATC/) RATCLIFFE O.  
PA (ADAM/) ADAM L J.  
PA (REUB/) REUBER T L.  
PA (KEDD/) KEDDIE J.  
PA (BROU/) BROUN P E.  
PA (PRIG/) PRIGIM M L.  
PA (DUBE/) DUBELL A N.  
PA (PINE/) PINEDA O.  
PA (YUGG/) YU G.  
PI Sherman BK, Riechmann JL, Jiang C, Heard JE, Hake V,  
PI Creelman RA, Ratcliffe O, Adam LJ, Reuber TL, Keddie J, Broun PE,  
PI Prigim ML, Dubell AN, Pineda O, Yu G;  
XX WPI: 2004-132245/13.  
DR N-PSDB; ADI44298.  
XX  
XX  
PT New transgenic plant comprising a recombinant polynucleotide of any one  
PT of more than 500 nucleotide sequences, useful in bioinformatic search  
PT methods.  
PS Disclosure; SEQ ID NO 2762; 435pp; English.  
XX  
XX The invention describes a transgenic plant comprising a recombinant  
XX polynucleotide of any one of more than 500 nucleotide sequences fully  
XX defined in the specification or its complement. The method of the  
XX invention can be used to produce a plant having altered traits such as:  
XX enhanced tolerance to abiotic stresses; glyphosphate tolerance; increased  
XX sensitivity; disease resistance; sugar sensing; early or late flowering;  
XX altered flower structure; change in stem bifurcations; altered branching  
XX pattern; reduced apical dominance; reduced trichome density; lack of  
XX trichomes; reduced ectopic trichome development; altered trichome  
XX development; increased in trichome number; altered stem morphology;  
XX increased root growth; increased root hairs; altered seed development;  
XX altered cell proliferation or cell differentiation; rapid development;  
XX premature senescence; increased necrosis; increase in seedling or plant  
XX size; decreased plant size; leaf morphology; seed morphology; seed  
XX biochemistry; increase in root anthocyanins; increase in plant  
XX anthocyanins, or alteration in light response or shade avoidance. The  
XX transgenic plant, polynucleotides and polypeptides are useful in  
XX bioinformatic search methods. This sequence represents a plant  
XX transcription factor related polynucleotide.  
SQ Sequence 209 AA;  
Query Match 29.5%; Score 402; DB 8; Length 209;  
Best Local Similarity 39.0%; Pred. No. 4.8e-25;  
Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;  
QY 1 MPTSDSEPRRIAMKENGVTVPISDQOQLPCPCDSSNTKCYNNYNFSGPRHFCAC 60  
Db 1 MP-SEPQTPPTPTVQSTAAVPPNLAEPLEPCPCNSTTTFYCYNNYNLAQPRYCKSC 59  
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Db 60 RRTWOGTLRDVVGSGGTRSSSKRRHSFSTATSSSSSVITTTQEBATTEA--S 116  
QY 118 QSSISNGVTHVTESDQKSLSLCSFTSTLHNNAATATGSGSVIGIG--FGIGL 175  
Db 117 QTKVTNLS-----GHGSPASLLGL-----GSGN-----GGLDYGFY 149  
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Db 191 GDSLIMPGLRISMQTNVVK 209  
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ID AAG36751 standard; protein; 226 AA.  
XX AAG36751;  
XX  
XX 18-OCT-2000 (first entry)  
XX  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 45084.  
XX Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
XX Arabidopsis thaliana.  
XX EP1033405-A2.  
XX  
XX 06-SEP-2000.  
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XX 25-FEB-2000; 2000EP-00301439.  
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XX 25-FEB-1999; 99US-0121825P.  
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Db      208 GDSLWPFLEISMQNDVK 226

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ID      AAG41702 standard; protein; 193 AA.
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AC      AAG41702;
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DT      18-OCT-2000 (first entry)
XX
DE      Arabidopsis thaliana protein fragment SEQ ID NO: 51918.
XX
KW      Protein identification; signal transduction pathway; metabolic pathway;
KM      hybridisation assay; genetic mapping; gene expression control; promoter;
XX      termination sequence.
OS      Arabidopsis thaliana.
XX      EPI033405-A2.
XX      06-SEP-2000.
XX      25-FEB-2000; 2000EP-00301439.
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PR	15-SEP-1999;	99US-0154018P.
PR	16-SEP-1999;	99US-0154039P.
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PR	28-OCT-1999;	99US-0161937P.
PR	29-OCT-1999;	99US-0162142P.

[illegible]

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PR 16-AUG-1999; 99US-0149368P.  
PR 17-AUG-1999; 99US-0149175P.  
PR 18-AUG-1999; 99US-0149426P.  
PR 20-AUG-1999; 99US-0149722P.  
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PR 20-AUG-1999; 99US-0149929P.  
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PR 10-SEP-1999; 99US-0153070P.  
PR 13-SEP-1999; 99US-0153758P.  
PR 15-SEP-1999; 99US-0154018P.  
PR 16-SEP-1999; 99US-0154039P.  
PR 20-SEP-1999; 99US-0154779P.  
PR 22-SEP-1999; 99US-0155139P.  
PR 23-SEP-1999; 99US-0155486P.  
PR 24-SEP-1999; 99US-0155659P.  
PR 28-SEP-1999; 99US-0156458P.  
PR 29-SEP-1999; 99US-0156596P.  
PR 04-OCT-1999; 99US-0157117P.  
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PR 21-OCT-1999; 99US-0160741P.  
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PR 21-OCT-1999; 99US-0160814P.  
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PR 22-OCT-1999; 99US-0160980P.  
PR 22-OCT-1999; 99US-0160981P.  
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PR 25-OCT-1999; 99US-0161404P.  
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PR 26-OCT-1999; 99US-0161360P.  
PR 26-OCT-1999; 99US-0161361P.  
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Query Match 27.7%; Score 377.5; DB 3; Length 194;  
Best Local Similarity 48.6%; Pred. No. 4; Ce-23;  
Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;







Best Local Similarity 48.8%; Pred. No. 4, 9e-23;  
Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;

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Db      25  EOEOELKCPRCDSPTNTEFCYNNYNNISQPHFACSCRRYMTKGALNVPVGGSRKQATK  84

QY      86  SRTCSNASSSVSGVVSNSNGVPLQTPVLPFSSISNGVTHT-----VTESDGKSA  138
Db      85  RSTSSSSSAASSSN--SSQKKTKKNDDPPDPFNSQKPPDLPRMLXGPIGQDVKG--  140

QY      139  LSLGSPFTSTLLNHNAAATATGSGSGVIGFGFGIGL--GSGPDDVSGFLG  187
Db      141  MEIGSGFSLLANN-----MQDLGGGGIMLDGSGMHPKMGGLG  179

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Search completed: November 3, 2005, 16:12:17  
Job time : 73 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 3, 2005, 16:09:31 ; Search time 15 Seconds  
(without alignments)  
1622.856 Million cell updates/sec

Title: US-10-509-691-2

Perfect score: 1363

Sequence: 1 MPTSDSGPRIRAMKPNVT.....SGEYFAMPDLSTTPGNSLK 253

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1033	75.8	195	2	T46072 DNA binding protei
2	1002	29.5	209	2	E96517 hypothetical prote
3	377.5	27.7	204	2	T52045 DoF zinc finger pr
4	327	24.0	328	2	T02046 prolamin box bindi
5	320.5	23.5	225	2	S59852 DNA-binding protei
6	318	23.3	194	2	T52044 dof zinc finger pr
7	317.5	23.3	399	2	T48267 hypothetical prote
8	316.5	23.2	339	2	H86210 hypothetical prote
9	314.5	23.1	262	2	T02203 finger protein DoF
10	312.5	22.9	311	2	D86409 hypothetical prote
11	309	22.7	385	2	E96669 protein FIN19.19 l
12	308.5	22.6	234	2	T02370 finger protein BBF
13	308	22.6	356	2	G84904 probable DOF zinc
14	306.5	22.5	320	2	B84689 probable DOF zinc
15	305	22.4	245	2	T47501 doF6 zinc finger p
16	304	22.3	259	2	G84685 probable DOF zinc
17	294.5	21.6	296	2	T47977 transcription fact
18	294.5	21.6	361	2	T13450 DNA-binding protei
19	293.5	21.5	238	2	S66358 DNA-binding protei
20	293.5	21.5	302	2	S59853 DNA-binding protei
21	290.5	21.3	278	2	F85012 hypothetical prote
22	290.5	21.3	575	2	T01552 hypothetical prote
23	290.5	21.3	238	2	T02373 finger protein BBF
24	286	21.0	330	2	T02525 probable DOF zinc
25	285	20.9	245	2	T05627 hypothetical prote
26	283.5	20.8	307	2	T47676 zinc finger protei
27	283	20.8	264	2	T50640 zinc finger protei
28	281.5	20.7	448	2	T45710 H-protein promoter
29	278.5	20.4	114	2	T02374 finger protein BBF

30	273	20.0	210	2	T10647 hypothetical prote
31	273	20.0	380	2	T09661 ascorbate oxidase
32	271	19.9	247	2	T09455 hypothetical prote
33	267.5	19.6	399	2	D96717 hypothetical prote
34	267.5	19.6	400	2	T51953 H-protein promoter
35	267	19.6	119	2	T02375 finger protein BBF
36	260.5	19.1	249	2	T04939 hypothetical prote
37	252.5	18.5	232	2	T10646 hypothetical prote
38	250.5	18.4	170	2	H84752 probable DOF zinc
39	178.5	13.1	194	2	T10645 hypothetical prote
40	123	9.0	1076	1	A35622 nuclear pore prote
41	122	9.0	963	2	T40290 hypothetical prote
42	113	8.3	749	2	T18488 trophinin - human
43	112.5	8.3	731	2	C70974 hypothetical glyci
44	112	8.2	1428	2	T08852 luciferin A - Califo
45	111.5	8.2	708	2	A53185 G-box-binding fact

#### ALIGNMENTS

##### RESULT 1

T46072 DNA binding protein - Arabidopsis thaliana (fragment)

N:Alternate names: protein T20E23.10

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 09-Jul-2004

C:Accession: T46072

R:Barques, M.; Perez-Derez, A.; Terol, J.; Torres, A.; Perez-Alonso, M.; Mewes, H.W.; Le

submitted to the Protein Sequence Database, December 1999

A:Reference number: 223020

A:Accession: T46072

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-195 <BAR>

A:Cross-references: UNIPROT:Q9M2R8; EMBL:AL133363

A:Experimental source: cultivar Columbia; BAC clone T20E23

C:Genetics:

A:Map position: 3

A>Note: T20E23.10

Query Match 75.8%; Score 1033; DB 2; Length 195;  
Best Local Similarity 100.0%; Pred. No. 4.7e-68;  
Matches 195; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	59	ACRRYTHGTLRDVPGGTRKSAKRRTCSNSSSVSGVSNQVPLQTPVLPQ	118
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QY	119	SSISNGVHTVTESDGKSAISLCSFTSTLLNHNAAATATGSGSVTGIGFGIGLSG	178
DB	61	SSISNGVHTVTESDGKSAISLCSFTSTLLNHNAAATATGSGSVTGIGFGIGLSG	120
QY	179	FDVVSFGIGRAMPFSTVGTATTNVSGNGHAAVPMATQFELBSNAGGFVSGEYF	238
DB	121	FDVVSFGIGRAMPFSTVGTATTNVSGNGHAAVPMATQFELBSNAGGFVSGEYF	180
QY	239	AMPDLSTTPGNSLK 253	
DB	181	AMPDLSTTPGNSLK 195	

##### RESULT 2

E96517 hypothetical protein F16N3.5 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004

C:Accession: E96517

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;

ansen, N.F.; Hughes, B.; Huizart, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Keri, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A66141; MUID:21016719; PMID:11130712  
A:Accession: E96517  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-209 <STO>  
A:Cross-references: UNIPROT:Q9SK97; GB:AB005173; NID:95668794; PIDN:AD46020.1; GSPDB:GN C:Genetics:  
A:Gene: P16N3.5  
A:Map position: 1

Query Match 29.5%; Score 402; DB 2; Length 209;  
Best Local Similarity 39.0%; Pred. No. 3e-22;  
Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;

QY 1 MPTSDSGEPRRIAMKPNGVTPISDQEQLPCEPCDSSNTKFCYNNYNFSGPRHFCAC 60  
D 1 MP-SEPNQTRPTROPSPRAAPRNLAEPPLCPRCNSTTTFCTYNNYNLAOPRYCKSC 59  
QY 61 RRYWTHGCTLRDVPVGGGTRK-SAKRSRTCSN--SSSSSVGVVSNNGVPLQTPVLPF 117  
D 60 RRYWTHGCTLRDVPVGGGTRSSSKRHRSFSTATSSSSSVITTTQEPATTEA---S 116  
QY 118 QSSISNGVTHVTSSDQKSLSCGFTSTLLNHNAAATTHSGSVIGIG--FGIGL 175  
D 117 QTKVTNLIIS-----GHGSFASLILGL-----GSGN---GGADYGFY 149  
QY 176 GSGFDVDSFG-IGRAMPFSTVGTATTNNGSGHHAVPMPTWQEGLESNAGGFFVS 234  
D 150 GYGLBEMSIGVLG-----SSVGERIPV--VDGCGD-----TWQGEIDGKSG----- 190  
QY 235 GEYFAMPDLSTITPGNSLX 253  
D 191 GDSLIWPGLEISMQTNIVK 209

## RESULT 3

Dof zinc finger protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Oct-2000 #sequence\_revision 20-Oct-2000 #text\_change 09-Jul-2004  
C:Accession: T52045  
R:Itagaki, T.; Kisu, Y.; Esaka, M.  
A:Submitted to the EMBL Data Library, September 1998  
A:Description: cDNA cloning and gene expression of Dof zinc finger protein in Arabidopsis  
A:Reference number: 225919  
A:Accession: T52045  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-204 <ITR>  
A:Cross-references: UNIPROT:O82156; EMBL:AB017565; PIDN:BAA33197.1  
C:Genetics:  
A:Gene: adof2

Query Match 27.7%; Score 377.5; DB 2; Length 204;  
Best Local Similarity 48.8%; Pred. No. 1.8e-20;  
Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;  
QY 26 QOEOLPCPCDSSNTKFCYNNYNFSGPRHFCACRRTWTHGTLRDVPVGGGTRKSAKR 85  
D 25 EQEOLKPCPCDSSNTKFCYNNYNFSGPRHFCACRRTWTHGTLRDVPVGGGTRKSAKR 84  
QY 86 SRTCSNSSSSSVGVVSNNGVPLQTPVLPPOSSISNGVTHT-----VTESDGKGA 138  
D 85 RSTSSSSASAPSN--SQNKTKTKNPPDPDPNRSQKRDLPPTMLVGFPIGDQDVHG-- 140  
QY 139 LSLGSGFTSTLLNHNAAATTHSGSVIGIGFGIGL-GSGFDVDSFGIGL 187  
D 141 MEIGSGFSSLIANN-----MQIGLGGGIMLDGSGMDHPGMGLG 179

RESULT 4  
T02046  
prolamin box binding factor - maize  
C:Species: Zea mays (maize)  
C:Date: 26-Feb-1999 #sequence\_revision 26-Feb-1999 #text\_change 09-Jul-2004  
C:Accession: T02046  
R:Vicente-Carvajosa, J.; Moose, S.P.; Parsons, R.L.; Schmidt, R.J.  
Proc. Natl. Acad. Sci. U.S.A. 94, 7685-7690, 1997  
A:Title: A maize zinc-finger protein binds the prolamin box in zein gene promoters and its  
A:Reference number: Z14511; MUID:97352860; PMID:9207153  
A:Accession: T02046  
A:Status: preliminary;  
A:Molecule type: mRNA  
A:Residues: 1-328 <VIC>  
A:Cross-references: UNIPROT:O24463; EMBL:U82230; NID:92393774; PIDN:AB70119.1; PID:9239  
C:Genetics:  
A:Gene: PBF

Query Match 24.0%; Score 327; DB 2; Length 328;  
Best Local Similarity 34.1%; Pred. No. 1.3e-16;  
Matches 88; Conservative 31; Mismatches 65; Indels 74; Gaps 9;

QY 5 DSGEPRRIAMKP-----NGVTVPIPSDQEQLPCEPCDSSNTKFCYNNYNFSGPRHFCAC 60  
D 31 EARDPKQTRAMPQIGSGGERKPRPOLPEALKPCRCDSNNTKFCYNNYNFSGPRHFCAC 90  
QY 61 RRYWTHGCTLRDVPVGGGTRKSAKR-----TCSNSSS---SVGVVSN----- 105  
D 91 RRYWTHGCTLRDVPVGGGTRKSAKR-----TCSNSSS---SVGVVSN----- 150  
QY 106 -----GVPDTPPLPFOSSISNGVTHVTSSDQKSLSCGFTSTLLNHNAAAT 157  
D 151 HMMWVPMWMTPTTNGLPF-----NVLEPTLPTGG-----GFDFTMDNQRSLS 197  
QY 158 AT-----HSGSGVIGIGF-----GIGLGSFGDVDSFGIGRAMPFSTVGT 199  
D 198 FTPLMSLPDSQGVPMVLAAGSEATPSEFLMLRGGIFPGS-----SSVNTS 241  
QY 200 TTTNNGSGHHAVPMPT 217  
D 242 LTVSGNNGMDKPSLPS 259

## RESULT 5

S59852  
DNA-binding protein Dof2 - maize (fragment)  
C:Species: Zea mays (maize)  
C:Date: 15-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 09-Jul-2004  
C:Accession: S59852  
R:Shuichi, Y.  
A:Submitted to the EMBL Data Library, June 1994  
A:Reference number: S59852  
A:Accession: S59852  
A:Molecule type: mRNA  
A:Residues: 1-225 <SHU>  
A:Cross-references: UNIPROT:Q41800; EMBL:X79934; NID:91061305; PIDN:CAA56287.1; PID:91061  
R:Yanagisawa, S.  
Nucleic Acids Res. 23, 3403-3410, 1995  
A:Title: A novel DNA-binding domain that may form a single zinc finger motif.  
A:Reference number: S59850; MUID:96032831; PMID:7567449  
A:Accession: S59850  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 13-85/96-119/211-225 <YAN>  
A:Cross-references: EMBL:X79934  
C:Keywords: zinc finger

Query Match 23.5%; Score 320.5; DB 2; Length 225;  
Best Local Similarity 31.0%; Pred. No. 2.7e-16;  
Matches 80; Conservative 37; Mismatches 80; Indels 61; Gaps 8;

QY	18	GATPAPISPOGQL-----PCPRCDSNTEFCYYNNYNFQPHPCACGRYTHGGTLADV	73
Db	2	CYPVPVAKEERPAAGDPCPRCGSRDTKCYNNINITSOPHLCKSCRNYTKGSLRN	61
QY	74	PVGCGTRKSAKRSTCNSSSSSVSGVSNNGVPLQTT-----PVLFPOST	121
Db	62	PVGCGTRKKS--SSSSSSSAAITTTTTTSTSPGAAPKATRKSKNSKRNRVAPADDPAPG	119
QY	122	SNGVHTVTESDGKSALSLCGSFSTLTLNNAATAATH--GSGSVIGIGFGIGLGSGF	179
Db	120	TDASTADVAST--APSATVVAASEKPSATEIAAAAATAVEKRPAPRVSVGAF-----	169
QY	180	DDVSFFGLGRAMPPSTVGATTNVGNSNGHHAVMPRTWQFEGLESNAGSGFVSGEYFA	239
Db	170	-----ADTSPAPDAGSGGVRELLPHPRFPFW-----PSCGDILGPYWG	207
QY	240	M-----PDLSITTP	248
Db	208	WGTSVLADTDPALFLNLIP	225

```

RESULT 6
T52044
dof zinc finger protein [imported] - Arabidopsis thaliana
C|Species: Arabidopsis thaliana (mouse-ear cress)
C|Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C|Accession: T52044
R|Itagaki, T.; Kieu, Y.; Esaka, M.
A|Submitted to the EMBL Data Library, September 1998
A|Description: cDNA cloning and gene expression of Dof zinc finger protein in Arabidopsis
A|Reference number: Z25919
A|Accession: T52044
A|Status: preliminary; translated from GB/EMBL/DBJ
A|Molecule type: mRNA
A|Residues: 1-194 <ITV>
A|Cross-references: UNIPROT:O82155; EMBL:AB017564; PDB:BAA33196.1
C|Genetic8:
;Gene: adof1

```

[illegible]

RESULT 7  
T48267  
probable zinc finger protein - *Arabidopsis thaliana*  
N/Alternate names: protein T22P11.50  
C/Species: *Arabidopsis thaliana* (mouse-ear cress)  
C/Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C/Accession: T48267  
R/Beyan, M.; Hilbert, H.; Braum, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancroft, submitted to the Protein Sequence Database, April 2000  
A/Reference number: Z24490  
A/Accession: T48267  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-399 <BEV>  
A/Cross-references: UNIPROT:Q9LZ56; EMBL:AL162971  
A/Experimental source: cultivar Columbia; BAC clone T22P11  
A/Genetics:

[illegible]

RESULT 8  
 H86210  
 hypothetical protein [imported] - Arabidopsis thaliana  
 C|Species: Arabidopsis thaliana (mouse-ear cress)  
 C|Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 A|Accession: H86210  
 R|Theologias, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
 Chih, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
 ansen, N.F.; Hughes, B.; Huizart, L.  
 Nature 408, 816-820, 2000  
 C.A.; Alt, J.H.; Li, Y.; Jenkins, J.; Johnson-Nopson, C.; Khan, S.; Khaykin, E.; Kim, C  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A|Authors: Salzberg, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A|Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A|Reference number: A86141; MUID:21016719; PMID:11130712  
 A|Accession: H86210  
 A|Status: Preliminary  
 A|Molecule type: DNA  
 A|Residues: 1-339 <SNO>  
 A|Cross-references: UNIPROT:Q9LQW7; GB:AF005172; NID:98439908; PIDN:AAF75094.1; GSPDB:GNQ  
 C|Genetics:  
 ;Map position: 1

Query Match	33.2%	Score 316.5;	DB 2;	Length 339;
Best Local Similarity	33.1%	Pred. No 8e-16;		
Matches	91;	Conservative 33;	Mismatches 78;	Indels 73; Gaps 14;

  

QY	30	LPCRCDSNNTKFCYNNYNFSGPRHFCCKACRRYTHGTLRDVPGGSTRKSAK----	84
Db	85	LKRCRCSSNTKFCYNNYNLTQPRHFCCKCRRYWTGGALRNPVGGGCRNNKKKG	144
QY	85	--RERTSNSSSSV-----SGVSNSSNCPLOTPTFLVLPSSISN-GVTHVTSBDK	135
Db	145	NLKSSSSSSKQSSSVNAQSPSSGQLRTNHQPPF--STLLYNLTQLGGTGLNLTATNGNQ	202
QY	136	-----GSAIS-----LGSFTSTLL-----NHAAATATHGSGSVIGIGFGIGSGF	179
Db	203	AHQGSSILMNSDLGFLHGRNTSTPMTGNIHENNNNNNNENNLMAVSGLSPALP----	257
QY	180	DVDSFGIGRAMMPSTYGTATTNVGSG-----HHAVPMATNQ-----	220
Db	258	DPTT-----GLYAAQNDG-----NIGNNVIGSGSTSMVDSRYQTPTPVMEEDPNLNL	307









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# OM protein - protein search, using sw model

Run on: November 3, 2005, 16:08:45 ; Search time 60 Seconds  
(without alignments)  
2159.267 Million cell updates/sec

Title: US-10-509-691-2

Perfect score: 1363  
Sequence: 1 MPTSDSGEPRIAMKPNQVT.....SGEYFAMPDLSTTPGNSLK 253

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1363	100.0	253	1	DP34_ARATH
2	651	47.8	225	1	DP58_ARATH
3	600.5	44.1	234	2	Q76KU9
4	402	29.5	209	1	DP16_ARATH
5	377.5	27.7	204	1	DP31_ARATH
6	340	24.9	290	2	Q76KV1
7	338.5	24.8	324	2	Q9M4G1
8	336.5	24.7	396	2	Q76KV0
9	329	24.1	333	2	Q92S77
10	328	24.1	360	2	Q7XS99
11	328	24.1	378	1	Q9SXG8
12	327	24.0	328	1	PBF_MAIZE
13	325.5	23.9	366	2	Q6EPG2
14	325.5	23.9	375	2	Q9SXG7
15	322	23.6	371	2	Q6F2W0
16	321.5	23.6	324	2	Q8LSB9
17	321.5	23.6	330	2	Q6RK62
18	321.5	23.6	330	2	Q9ZRX2
19	321.5	23.6	355	2	Q84T97
20	320.5	23.5	225	2	Q41800
21	320.5	23.5	307	1	DP54_ARATH
22	320	23.5	372	1	DP56_ARATH
23	318	23.3	194	1	DP17_ARATH
24	317.5	23.3	331	2	Q6ICV3
25	317.5	23.3	399	1	DP51_ARATH
26	317	23.3	359	1	DP51_ARATH
27	316.5	23.2	331	1	DP11_ARATH
28	316	23.2	341	2	Q76KV7
29	315	23.1	262	2	Q7X170
30	314.5	23.1	262	2	Q82027
31	314.5	23.1	296	2	Q76KV2

32	313.5	23.0	290	2	Q65XV0	Q65XV0
33	312.5	22.9	311	1	DP14_ARATH	Q9FZ44 arabidopsis
34	312	22.9	276	2	Q6ZB01	Q6ZB01 oryza sativ
35	311.5	22.9	340	1	DP22_ARATH	Q9ZV33 arabidopsis
36	309	22.7	352	1	DP18_ARATH	Q84J98 arabidopsis
37	308.5	22.6	234	2	Q43570	Q43570 nicotiana t
38	308.5	22.6	472	2	Q8RVK0	Q8RVK0 hordeum vul
39	308.5	22.6	472	2	Q8RVK1	Q8RVK1 hordeum vul
40	308	22.6	369	1	DP25_ARATH	Q9ZPY0 arabidopsis
41	306.5	22.5	257	1	DP53_ARATH	Q84T98 arabidopsis
42	305	22.4	245	1	DP32_ARATH	Q9M166 arabidopsis
43	304	22.3	288	1	DP21_ARATH	Q81E43 arabidopsis
44	303.5	22.3	282	2	Q6Z345	Q6Z345 oryza sativ
45	303.5	22.3	282	2	Q9SXG5	Q9SXG5 oryza sativ

## ALIGNMENTS

RESULT 1  
DP34\_ARATH STANDARD; PRT; 253 AA.  
ID DP34\_ARATH  
AC Q93088; Q9M2R8;  
DT 25-OCT-2004 (Rel. 45, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-JAN-2005 (Rel. 46, Last annotation update)  
DE DoF zinc finger protein DOF3.4 (AtDOF3.4) (OBF binding protein 1).  
GN Name=DOF3.4; Synonyms=OBP1; OrderedLocNames=At3g50410;  
GN ORFNames=P101.250;  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
OX NCBI\_TaxID=3702;  
RX [1]  
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INTERACTION WITH OBP4 AND  
OBP5.  
RC STRAIN=cv. Columbia;  
RX Zhang B., Chen W., Foley R.C., Buettner M., Singh K.B.,  
RA "Interactions between distinct types of DNA binding proteins enhances  
RT binding to ocs-element promoter sequences";  
RL Plant Cell 7:2241-2252(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=96351937; PubMed=8718629;  
RA Salanoubat M., Lemcke K., Rieger M., Ansozge W., Unseld M.,  
RA Fattmann B., Valle G., Bloeker H., Perez-Alonso M., Obermayer B.,  
RA Delgeny M., Boutry M., Grivell L.A., Maché R., Puigdemont P.,  
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brottier P.,  
RA Wincker P., Catalicio L., Weissenbach J., Saurin W., Querier F.,  
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
RA Wumbsch E., Dizonet H., Erfle H., Jordan N., Bangert S.,  
RA Wiedemann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,  
RA Verzi A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,  
RA Conrad A., Hornischer K., Kauer G., Loenert T.-H., Nordiek G.,  
RA Reichelt J., Scharfe M., Schoen O., Baynes M., Terol J., Climent J.,  
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,  
RA Cooke R., Landie M., Berger-Liaou C., Purnelle B., Masuy D.,  
RA de Haan M., Maaree A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,  
RA Montfort A., Argitrou A., Flores M., Lignori R., Vitale D.,  
RA Mannheim G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,  
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Talon L.J., Jenkins J.,  
RA Rooney T., Rizzo M., Walte A., Uteback T., Fujii C.Y., Shea T.P.,  
RA Cressy T.H., Haas B., Walte R., Wu D., Peterson J., Van Aken S.,  
RA Pal G., Miltner J., Sellier P., Gill J.E., Feldlyum T.V.,  
RA Prusse D., Lin X., Nieman W.C., Salzberg S.L., White O., Venter J.C.,  
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
RA Sasano S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,  
RA Kiyokawa C., Kohara M., Matsumoto M., Matsumoto A., Mutaki A.,  
RA Nakayama S., Nakazaki N., Shino S., Takeuchi C., Wada T.,  
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;

```

RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana."
RL Nature 408:820-822(2000).
RN (3)
RP TISSUE SPECIFICITY, AND INDUCTION.
RX PubMed=10758484;
RA Kang H.-G., Singh K.B.;
RT "Characterization of salicylic acid-responsive, Arabidopsis Dof domain
RT proteins: overexpression of OBP3 leads to growth defects."
RL Plant J. 21:329-339(2000).
RN (4)
RP GENE FAMILY, AND NOMENCLATURE.
RX PubMed=12475498;
RA Yanagisawa S.;
RT "The Dof family of plant transcription factors."
RL Trends Plant Sci. 7:555-560(2002).
CC -1- FUNCTION: Transcription factor that binds specifically to a 5'-
CC AA[AG]G-3' consensus core sequence. Enhances the DNA binding of
CC OBP transcription factors to OCS elements.
CC -1- SUBUNIT: Interacts with OBP4 or OBP5.
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- TISSUE SPECIFICITY: Constitutively expressed in the whole plant.
CC -1- INDUCTION: By auxin and salicylic acid (SA).
CC -1- SIMILARITY: Contains 1 Dof-type zinc finger.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a
CC frameshift in position 4.
-----
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-----
DR EMBL: X89192; CAAG1485.1; ALT_FRAME.
DR EMBL: AL132976; CAB88324.1; -.
DR FTR: T46072; T46072.
DR TRANSFAC: T02694; -.
DR InterPro: IPR003851; Znf_Dof.
DR Pfam: PFO2701; zf-Dof; 1.
DR PROSITE: PS01361; ZF_DOF_1; 1.
DR PROSITE: PS50884; ZF_DOF_2; 1.
DR DNA-binding; Metal-binding; Nuclear protein; Trans-acting factor;
DR Transcription regulation; Zinc; Zinc-finger.
FT ZN_FING 30 84 Dof-type.
FT DOMAIN 90 98 Poly-Ser.
FT CONFLICT 155 155 A->R (in Ref. 1).
SQ SEQUENCE 253 AA; 26382 MW; 3A64EA3FECFA5D1 CRC64;
Query Match 100.0%; Score 1363; DB 1; Length 253;
Best Local Similarity 100.0%; Pred. No. 5.5e-93;
Matches 253; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPTSDSEPPRIAMKPNVTVPIISDQEQLPFCPCDSSNTKFCYNNYNSQPRHFKAC 60
DB 1 MPTSDSEPPRIAMKPNVTVPIISDQEQLPFCPCDSSNTKFCYNNYNSQPRHFKAC 60
QY 61 RRYVTHGTLRDVPGVGGTRKSAKRSPRTCSNSSSSSVGVVNSNGVPLQTTPLVFOSS 120
DB 61 RRYVTHGTLRDVPGVGGTRKSAKRSPRTCSNSSSSSVGVVNSNGVPLQTTPLVFOSS 120
QY 61 RRYVTHGTLRDVPGVGGTRKSAKRSPRTCSNSSSSSVGVVNSNGVPLQTTPLVFOSS 120
DB 61 RRYVTHGTLRDVPGVGGTRKSAKRSPRTCSNSSSSSVGVVNSNGVPLQTTPLVFOSS 120
QY 121 ISNGVTHVTESDGKSAISLCSFSTLLNHNAAATATHGSGSVIGIGFGIGLGSQFD 180
DB 121 ISNGVTHVTESDGKSAISLCSFSTLLNHNAAATATHGSGSVIGIGFGIGLGSQFD 180
QY 121 ISNGVTHVTESDGKSAISLCSFSTLLNHNAAATATHGSGSVIGIGFGIGLGSQFD 180
DB 121 ISNGVTHVTESDGKSAISLCSFSTLLNHNAAATATHGSGSVIGIGFGIGLGSQFD 180
QY 181 DVSGGLRAMWPFSTVGTATTTNGSNGCHRAVPMPTWQEGLESNAGGFGVSGEYFAW 240
DB 181 DVSGGLRAMWPFSTVGTATTTNGSNGCHRAVPMPTWQEGLESNAGGFGVSGEYFAW 240
QY 241 PDLSTTPGNSLK 253
DB 241 PDLSTTPGNSLK 253

```

```

RESULT 2
ID DPF58_ARATH STANDARD; PRT; 225 AA.
AC Q9FGD6;
DT 25-JAN-2005 (Rel. 46, Created)
DT 25-JAN-2005 (Rel. 46, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Hypothetical Dof zinc finger protein DPF5.8 (AtDof5.8).
GN Name=Dof5.8; OrderedAccession=At5g66940; ORFNames=KRA10.1;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Kaneke T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP GENE FAMILY, AND NOMENCLATURE.
RX PubMed=12475498;
RA Yanagisawa S.;
RT "The Dof family of plant transcription factors."
RL Trends Plant Sci. 7:555-560(2002).
CC -1- FUNCTION: Transcription factor that binds specifically to a 5'-
CC AA[AG]G-3' consensus core sequence (By similarity).
CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
CC -1- SIMILARITY: Contains 1 Dof-type zinc finger.
-----
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-----
DR EMBL: AB026640; BAB08933.1; -.
DR InterPro: IPR003851; Znf_Dof.
DR Pfam: PFO2701; zf-Dof; 1.
DR PROSITE: PS01361; ZF_DOF_1; 1.
DR PROSITE: PS50884; ZF_DOF_2; 1.
DR DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;
DR Trans-acting factor; Transcription regulation; Zinc; Zinc-finger.
FT ZN_FING 32 86 Dof-type.
SQ SEQUENCE 225 AA; 24117 MW; 313D80AC406FC09D CRC64;
Query Match 47.8%; Score 651; DB 1; Length 225;
Best Local Similarity 55.5%; Pred. No. 2e-40;
Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;
QY 1 MPTSDSEPPRIAMKPNG---VTVPISDQEQLPFCPCDSSNTKFCYNNYNSQPRHF 56
DB 1 MPTSDSEPPRIAMKPNG---VTVPISDQEQLPFCPCDSSNTKFCYNNYNSQPRHF 56
QY 1 MPTSDSEPPRIAMKPNG---VTVPISDQEQLPFCPCDSSNTKFCYNNYNSQPRHF 56
DB 1 MPTSDSEPPRIAMKPNG---VTVPISDQEQLPFCPCDSSNTKFCYNNYNSQPRHF 56
QY 57 CKAKCRVTHGTLRDVPGVGGTRKSAKRSPRTCSNSSSSSVGVVNSNGVPLQTTPLV 116
DB 57 CKAKCRVTHGTLRDVPGVGGTRKSAKRSPRTCSNSSSSSVGVVNSNGVPLQTTPLV 116
QY 57 CKAKCRVTHGTLRDVPGVGGTRKSAKRSPRTCSNSSSSSVGVVNSNGVPLQTTPLV 116
DB 57 CKAKCRVTHGTLRDVPGVGGTRKSAKRSPRTCSNSSSSSVGVVNSNGVPLQTTPLV 116
QY 117 POSSISNGVTHVTESDGKSAISLCSFSTLLNHNAAATATHGSGSVIGIGFGIGL 176
DB 117 POSSISNGVTHVTESDGKSAISLCSFSTLLNHNAAATATHGSGSVIGIGFGIGL 176
QY 115 POSSISNGVTHVTESDGKSAISLCSFSTLLNHNAAATATHGSGSVIGIGFGIGL 167
DB 115 POSSISNGVTHVTESDGKSAISLCSFSTLLNHNAAATATHGSGSVIGIGFGIGL 167
QY 177 SG--FDVSGFLGRAMWPFSTVGT--ATTNVSNGCHRAVPMPTWQEGLESNAGG 232
DB 177 SG--FDVSGFLGRAMWPFSTVGT--ATTNVSNGCHRAVPMPTWQEGLESNAGG 232
QY 168 HGSYEDVRYGGIGITVWPFSSGATDAATTS-----HIAQIPATWQEGSSKV--GF 218
DB 168 HGSYEDVRYGGIGITVWPFSSGATDAATTS-----HIAQIPATWQEGSSKV--GF 218
QY 233 VSGEYFA 239

```

Db 219 VSGDYVA 225

## RESULT 3

076KU9 PRELIMINARY; PRT; 234 AA.

DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DE DNA binding with one finger 5 protein.  
 GN Name=PsdoF5;  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eucosida 1; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
 OC NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Epilcotyls;  
 RA Nakamura N., Marutani M., Senematsu S., Toyoda K., Inagaki Y.-S.,  
 RA Shiraishi T., Ichinose Y.,  
 RT "Phylogenetic Classification of DoF-type Transcription Factors in Pea  
 (Pisum sativum).";  
 RL Plant Biotechnol. 20:247-253 (2003).  
 DR EMBL: AB087850; BAC81662.1;  
 DR GO: GO:0003677; F:DNA binding; IEA.  
 DR InterPro: IPR003851; Znf\_Dof.  
 DR Pfam: PF02701; ZF-Dof; 1.  
 DR PROSITE: PS01361; ZF\_DOF\_1; UNKNOWN\_1.  
 DR PROSITE: PS50884; ZF\_DOF\_2; 1.  
 SQ SEQUENCE 234 AA; 24607 MW; C28B6801EBE7370B CRC64;

Query Match 44.1%; Score 600.5; DB 2; Length 234;

Best Local Similarity 50.8%; Pred. No. 1.1e-36;

Matches 134; Conservative 32; Mismatches 57; Indels 41; Gaps 13;

QY 1 MPTSSGGERRIAMKNGVTVPISDQOQLPCPRCDSSNTKRCYNNNNYFSQPRHCRAC 60  
 DB 1 MPSSSGSSRR-SIRPQNRPAPAPBQENLPCCPRCDSTTKCYNNNNYFSQPRHCRAC 59  
 QY 61 RRYWTHGGLRDVDPVGGGTRKSAKRSRT--CNSSSSSVGVNSNGVPLQTTVPVLPFQ 118  
 DB 60 RRYWTHGGLRDVDPVGGGTRKSAKRSRTTHAVTSSSSSAATYS----APEQNYBSMPRI 115  
 QY 119 SSIS---NGVTHVTESDGKGA-LSLCGSPFTSTLLNNAATAATHGSGSVIGGFGIG 174  
 DB 116 QGSGSPYGGV-----DQEGKQNNMSVCGSPTS-LLNNN-----PQNSGFLALGGFGIG 162  
 QY 175 LGSFDDVVSFLGRAMPSTVGTATTNNGSNGGHHAVPMPA-----TWQFEGLESNAG 229  
 DB 163 LGHGIGDGGFGIGRE-WSPF--GMMDGSNMG-----VPVSSGIGNSWOLEGGETFRV 212  
 QY 230 GGFVSGEYFAMPDLITTPGNSLK 253  
 DB 213 GG--GGDCTSWPGLAISTFGNGLK 234

## RESULT 4

DF16 ARATH STANDARD; PRT; 209 AA.

DT 25-JAN-2005 (Rel. 46, Created)  
 DT 25-JAN-2005 (Rel. 46, Last sequence update)  
 DE Hypothetical DoF zinc finger protein DOF1.6 (AtDOF1.6).  
 GN Name=DOF1.6; OrderedlocusNames=At1g947655; ORFNames=FLN3.5;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eucosida 1; Brassicales; Brassicaceae; Arabidopsia.  
 OC NCBI\_TaxID=3702;

RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.R., Cressy T.H., Dewar K.,  
 RA Dunn P., Eguu P., Feldblyum T.V., Feng U.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Iwros J.S., Maiti R., Marzilli A.,  
 RA Miltschev J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,  
 RA Pail G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Utecherback T., Van Aken S., Vayberg M., Vysotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 thaliana".  
 RL Nature 408:816-820 (2000).  
 RN [2]  
 RP GENE FAMILY, AND NOMENCLATURE.  
 RX PubMed=12475498;  
 RA Yanagiawa S.;  
 RT "The DoF family of plant transcription factors.";  
 RL Trends Plant Sci. 7:555-560 (2002).  
 CC -I- FUNCTION: Transcription factor that binds specifically to a 5'-  
 AA[AG]G-3' consensus core sequence (By similarity).  
 CC -I- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -I- SIMILARITY: Contains 1 DoF-type zinc finger.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: AC007519; AAD46020.1; -  
 DR PIR: B96517; B96517.  
 DR InterPro: IPR003851; Znf\_Dof.  
 DR Pfam: PF02701; ZF-Dof; 1.  
 DR PROSITE: PS01361; ZF\_DOF\_1; 1.  
 DR PROSITE: PS50884; ZF\_DOF\_2; 1.  
 KW DNA-binding; Hypothetical protein; Metal-binding; Nuclear protein;  
 KW Trans-acting factor; Transcription regulation; Zinc; Zinc-finger.  
 FT ZN\_FING 29  
 FT DOMAIN 81  
 FT DOMAIN 81 101 Ser-rich.  
 FT DOMAIN 126 191 Gly-rich.  
 SQ SEQUENCE 209 AA; 22292 MW; 0BC93B44C49F09E CRC64;

Query Match 29.5%; Score 402; DB 1; Length 209;

Best Local Similarity 39.0%; Pred. No. 4.8e-22;

Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;

QY 1 MPTSDGGERRIAMKNGVTVPISDQOQLPCPRCDSSNTKRCYNNNNYFSQPRHCRAC 60  
 DB 1 MP-SEPNQRTPRVGPSTAAVPPMLAPLPPEPRCNSITTKRCYNNNNLQAPRYCKSC 59  
 QY 61 RRYWTHGGLRDVDPVGGGTRK-SAKRSYCSN--SSSSSVGVNSNGVPLQTTVPVLPF 117  
 DB 60 RRYWTHGGLRDVDPVGGGTRSSSRHRSFSTATSSSSSVITTTQEPATYBA---S 116  
 QY 118 OSSISNGVTHVTESDGKSA-LSLCGSPFTSTLLNNAATAATHGSGSVIGG--FGIGL 175  
 DB 117 QTKVNLIS-----GGSGPASILGL-----GSGN-----GGLDYGRGY 149  
 QY 176 GSGFDDVVSFLGRAMPSTVGTATTNNGSNGGHHAVPMPATWQFEGLESNAGGFRVS 234

Db 150 GYGEEMSIGYLGD-----SSVGEIPV--VDGCGD-----TWIGIEBGSG----- 190

Qy 235 GEFAMPDLSITTPGNSLK 253

Db 191 GDSLWPGLEISMQRNDVK 209

RESULT 5

DF31 ARATH STANDARD; PRT; 204 AA.

AC 094AR6; 082156;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Dof zinc finger protein DOF3.1 (AtDOF3.1).

GN Name=DOF3.1; Synonyms=ADOZF; OrderedLocustNames=At3g21270;

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI\_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Seedling;

RA Itagaki T., Kisu Y., Saaka M.,

RT "cDNA cloning and gene expression of Dof zinc finger protein in Arabidopsis thaliana."

RL Submitted (SEP-1998) to the EMBL/Genbank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RA MEDLINE=20277480; PubMed=10819329;

RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.,

RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty pl and TAC clones."

RT clone#,"

RL DNA Res. 7:131-135 (2000).

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RA MEDLINE=22954850; PubMed=14593172; DOI=10.1126/science.1088305;

RA Yamada K., Lim J., Dale J.M., Chen H., Shim P., Palm C.J.,

RA Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

RA Karlin-Newmann G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,

RA Miralanda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

RA Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,

RA Araiawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

RA Chao Q., Choy N., Ejima A., Goldsmith A.D., Gurjal M., Hansen N.F.,

RA Hayashizaki Y., Johnson-Hopson C., Hsuan V.W., Iida K., Karnes M.,

RA Khan S., Koeseema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

RA Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,

RA Satou M., Tamse R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,

RA Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.,

RT "Empirical analysis of transcriptional activity in the Arabidopsis genome."

RL Science 302:842-846 (2003).

RN [4]

RP GENE FAMILY, AND NOMENCLATURE.

RX PubMed=12475498;

RA Yanagisawa S.,

RT "The Dof family of plant transcription factors."

RL Trends Plant Sci. 7:555-560 (2002).

CC - FUNCTION: Transcription factor that binds specifically to a 5'-

CC AA[AG]G-3' consensus core sequence (by similarity).

CC - SUBCELLULAR LOCATION: Nuclear (Probable).

CC - SIMILARITY: Contains 1 Dof-type zinc finger.

CC -----

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CC -----

DR EMBL; AB017565; BAA33197.1; -

DR EMBL; AB023045; BAB01720.1; -

DR EMBL; AY045847; AAK76521.1; -

DR EMBL; AY150391; AAN12936.1; -

DR PIR; T52045; T52045.

DR InterPro; IPR003851; ZnF\_Dof.

DR Pfam; PF02701; Zf-Dof; 1.

DR PROSITE; PS01361; ZF\_DOF\_1; 1.

DR PROSITE; PS00884; ZF\_DOF\_2; 1.

KW DNA-binding; Metal-binding; Nuclear protein; Trans-acting factor;

KW Transcription regulation; Zinc; Zinc-finger.

FT ZN FING 29

FT CONFLICT 97 97 S->T (in Ref. 3; AAK76521).

SO SEQUENCE 204 AA; 22530 MW; 4D6FBD4BC51759 CRC64;

Query Match 27.7%; Score 377.5; DB 1; Length 204;

Best Local Similarity 48.8%; Pred. No. 3e-20;

Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;

Qy 26 QOEQLPCPRCDSSNTKCYNNYVFSQPRHFCACRRTWTHGTLRDVYVGGGTRKSAKR 85

Db 25 EQEQLKCPDCDSPTKFCYNNYVLSQPRHFCCKRCRYWTKGALRVNVPVGGGSRKATK 84

Qy 86 SRTCSNSSSSVSGVNSNGVPLQTTPLVPESSISNGVTH-----VTESDGKSA 138

Db 85 RSTSSSSSASPSN--SSQKKTGNPPDPDPFRNSQRPDLPTMLYGFPGDDVKG-- 140

Qy 139 LSLGFSFTSLNLNNAATHTGSGSVIGIGFGIGL-GSGFDDVSFGLG 187

Db 141 MEIGSGFSLLANN-----MQLGIGGGIMLDGSGMDHPGMGLG 179

RESULT 6

Q76KV1

AC 076KV1 PRELIMINARY; PRT; 290 AA.

DT 05-JUL-2004 (TRENDSrel. 27, Created)

DT 05-JUL-2004 (TRENDSrel. 27, Last sequence update)

DT 05-JUL-2004 (TRENDSrel. 27, Last annotation update)

DE DNA binding with one finger 3 protein.

GN Name=PSDOF3;

OS Pisum sativum (Garden pea).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.

OX NCBI\_TaxID=3888;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Epicytyle;

RA Nakamura N., Marutani M., Sanematsu S., Toyoda K., Inagaki Y.-S.,

RT "Phylogenetic Classification of Dof-type Transcription Factors in Pea (Pisum sativum)."

RL Plant Biotechnol. 20:247-253 (2003).

DR EMBL; AB087848; BAC81660.1; -

DR GO; GO:0003577; F-DNA binding; IEA.

DR InterPro; IPR003851; ZnF\_Dof.

DR Pfam; PF02701; ZF-Dof; 1.

DR PROSITE; PS01361; ZF\_DOF\_1; UNKNOWN\_1.

DR PROSITE; PS00884; ZF\_DOF\_2; 1.

SO SEQUENCE 290 AA; 31740 MW; 9637CF3508582DA CRC64;

Query Match 24.9%; Score 340; DB 2; Length 290;

Best Local Similarity 34.8%; Pred. No. 2.6e-17;

Matches 79; Conservative 40; Mismatches 94; Indels 14; Gaps 4;

Qy 26 QOEQLPCPRCDSSNTKCYNNYVFSQPRHFCACRRTWTHGTLRDVYVGGGTRKSAKR 85

Db 17 QOEQLKCPDCDSNTKFCYNNYVLSQPRHFCACRRTWTHGTLRVNVPVGGGTRKRNKR 76

QY 86 SRTCSNSSSSVSGVNSNGVLPQTTPVLPFOSSISNGVTHVTESD-----GKGSAL 139  
 DB 77 SRTSSNGPSTITTLTKR-----PISTIETATSSNSSPSSTSSNNHNPMPYGLSSIN 131  
 QY 140 SLICG-SFTSTLLNHNAAATATATGSSVIGIGFGIGLGSFPDVSF--GLGRAMPFSTV 196  
 DB 132 NPCDNLPFRSRFNITSLRSLSTSSGYDLQPOMNFGLGFGSSGFENNNGYTNFNSTNNYDSI 191  
 QY 197 GTATTNNNGSGHHAVPMPTWQFEGLESNAGGVSCEVFAMPDL 243  
 DB 192 FSSSTSSANNISVMPSSVLSSTLLQHKFDDGLKYGSDAGSNGAFQDL 238

## RESULT 7

Q9MAG1 PRELIMINARY; PRT; 324 AA.  
 AC Q9MAG1.  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE DoF zinc finger protein.  
 GN Name=dozf1.  
 OS Solanum tuberosum (Potato).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Solanales; Solanaceae; Solanum.  
 NCBI\_TaxID=4113;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Epidermal fragments;  
 RA Plesch G., Ehrhardt T., Mueller-Roeber B.;  
 RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: AJ242853; CAB69831.1; --  
 DR TRANSFAC; T05500; --  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR InterPro; IPR003851; ZnF DoF.  
 DR Pfam; PF02701; zf-Dof; 1.  
 DR PROSITE; PS01361; ZF DOF 1; UNKNOWN\_1.  
 DR PROSITE; PS50884; ZF DOF 2; 1.  
 SQ SEQUENCE 324 AA; 35057 MW; 62E79B2214395C25 CRC64;

Query Match 24.8%; Score 338.5; DB 2; Length 324;  
 Best Local Similarity 33.0%; Pred. No. 3.8e-17;  
 Matches 93; Conservative 35; Mismatches 99; Indels 55; Gaps 13;

QY 9 PRRIIMKNGV-----TVPISDQQLPCPRCDSSNTFCYNNYNSQPRHF 56  
 DB 40 PMQVAGSPGISIRPGSMVDRARLAKIPL--PEAGLKCPCRDSTNTKFCYFNNTNLSQPRHF 97  
 QY 57 CKACRRYTHGGTLDVPGGSTRKAKRSRTCSNSSSVSGVNSNGVLPQTTPVL 116  
 DB 98 CKTCRRYTRGAGLSPVGGGCRKN-KRKSNNNNSSKTAAGSVNNTTISGTSNAS 156  
 QY 117 PQS--SISNGVTHVTESDGKSALSLCSFTSTLLNHNAAA-----TATGSGSVIG 167  
 DB 157 PSSCSTEIMNGHHSHQPPQ--LTPMLAARQN--LNNHGGFQRPPLVSHHNGTGA 212  
 QY 168 IG-----GFGIGL-----GSGFDD--VSFGLGRAMPF--STYGTATTTNV 204  
 DB 213 LGHHHEMFQIGSSNTNTNLLPVRPGGSDHQRRLSLAANTNLVYFQHDGQIHSSSV 272  
 QY 205 GSN--GSHAVPMPTWQFEGLESNAGGVSCEVFAMPDL 244  
 DB 273 NNNNINAHDDGALNTKQPLGMENTNTQYMGSN--ANTGFS 312

## RESULT 8

Q76KV0 PRELIMINARY; PRT; 396 AA.  
 AC Q76KV0.  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE DNA binding with one finger 4 protein.

GN Name=Padof4;  
 OS Pisum sativum (Garden pea).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC Eurosids I; Fabales; Fabaceae; Papilionoideae; Viciae; Pisum.  
 NCBI\_TaxID=3888;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=epicotyls;  
 RA Nakamura N., Marutani M., Sanematsu S., Toyoda K., Inagaki Y.-S.,  
 RA Shiraishi T., Ichinose Y.;  
 RT "Phylogenetic Classification of DoF-type Transcription Factors in Pea  
 (Pisum sativum)";  
 RL Plant Biotechnol. 20:247-253 (2003).  
 DR EMBL; AB087849; BAC81661.1; --  
 DR GO; GO:0003677; F:DNA binding; IEA.  
 DR InterPro; IPR003851; ZnF DoF.  
 DR Pfam; PF02701; zf-Dof; 1.  
 DR PROSITE; PS01361; ZF DOF 1; UNKNOWN\_1.  
 DR PROSITE; PS50884; ZF DOF 2; 1.  
 SQ SEQUENCE 396 AA; 43073 MW; 97DF573A5E86ED9F CRC64;

Query Match 24.7%; Score 336.5; DB 2; Length 396;  
 Best Local Similarity 31.0%; Pred. No. 6.6e-17;  
 Matches 98; Conservative 26; Mismatches 95; Indels 97; Gaps 11;

QY 6 GSEPRRIIMKNGVTPVPSDQQLPCPRCDSSNTFCYNNYNSQPRHFCKARRWT 65  
 DB 35 SSTGNRVMEKPGQEL--LQQOQQLRCPCRDSSNTFCYNNYNSLTPRHFCKARRWT 92  
 QY 66 HGGTLDVPGGSTRKAKRSR---TGSNS-----SSSVSGVNSNGVLPQTTP 113  
 DB 93 RGGTLRNVVGGGCKKRLKRLPYPCSNNNNIDPSAPSSSTPSSVANPV--PSSQSQ 151  
 QY 114 VLFPOS--SISNGVTHVTESDGKSALSLCSFTSTLLNHNAAATATGSGSVIG 169  
 DB 152 QQQQOQHHSFDIAATNSNINNTMLYGCNSCHVYNNPFTTRFRSTTRVNPASGYNDLPQN 211  
 QY 170 GFGIGLGSF-----DVVSFGLGRAMPFST-----VGTATT 201  
 DB 212 GIGLGFSSGILMSAAGEVNLNHHNHHHDEGSYRNG-----FSTSNNNYSISIGSSST 266  
 QY 202 TN-----VGSNGG-----HHAIVPWA----- 217  
 DB 267 TTPVMASLISSTLLQOKMGTGGGIGKGGGGGGDDDFPHHQMDSKVKLGBGLQNR 326  
 QY 218 -TWQFEGLESNAGGF 232  
 DB 327 DQNMNNNLNNGGANVF 342

## RESULT 9

Q9ZS77 PRELIMINARY; PRT; 333 AA.  
 AC Q9ZS77.  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE DNA binding protein.  
 GN Name=BBP1;  
 OS Hordeum vulgare (Barley).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 OC Triticeae; Hordeum.  
 NCBI\_TaxID=4513;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99024959; PubMed=9807827;  
 RA Mena M., Vicente-Carbajosa J., Schmidt R.J., Carbonero P.;  
 RT "An endosperm-specific DoF protein from barley, highly conserved in  
 wheat, binds to and activates transcription from the prolamin-box of a  
 native B-hordein promoter in barley endosperm.";









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OM protein - protein search, using sw model

Run on: November 3, 2005, 16:10:40 : Search time 43 Seconds  
(without alignments)  
439.214 Million cell updates/sec

Title: US-10-509-691-2  
Perfect score: 1163  
Sequence: 1 MPTSDSGPRRIAMKPNVGT.....SGEYFAMPDLSTTPGSLK 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	298.5	21.9	214	US-09-598-401C-70	Sequence 70, Appl
2	253.5	18.6	60	US-09-434-840-6	Sequence 6, Appl
3	129	9.5	712	US-09-248-796A-14274	Sequence 14274, A
4	123	9.0	1160	US-08-808-599A-24	Sequence 24, Appl
5	119	8.7	674	US-08-317-552A-3	Sequence 3, Appl
6	119	8.7	674	US-08-439-818A-3	Sequence 3, Appl
7	119	8.7	674	US-08-751-965-3	Sequence 3, Appl
8	119	8.7	674	US-08-738-975-3	Sequence 3, Appl
9	119	8.7	674	US-08-728-626-3	Sequence 3, Appl
10	119	8.7	674	US-08-808-599A-3	Sequence 3, Appl
11	113	8.3	749	US-08-317-552A-2	Sequence 2, Appl
12	113	8.3	749	US-08-439-818A-2	Sequence 2, Appl
13	113	8.3	749	US-08-751-965-2	Sequence 2, Appl
14	113	8.3	749	US-08-738-975-2	Sequence 2, Appl
15	113	8.3	749	US-08-728-626-2	Sequence 2, Appl
16	113	8.3	749	US-08-808-599A-2	Sequence 2, Appl
17	108.5	8.0	374	US-09-248-796A-17283	Sequence 17283, A
18	103.5	7.6	553	US-09-242-913B-13	Sequence 13, Appl
19	103	7.6	975	US-09-328-352-4764	Sequence 4764, Ap
20	102.5	7.5	449	US-08-927-394-2	Sequence 2, Appl
21	102.5	7.5	449	US-09-538-092-1372	Sequence 1372, Ap
22	102.5	7.5	449	US-09-949-016-6604	Sequence 6604, Ap
23	102.5	7.5	563	US-09-949-016-10153	Sequence 10153, A
24	102	7.5	231	US-09-248-796A-14281	Sequence 14281, A
25	102	7.5	353	US-08-687-702-37	Sequence 37, Appl
26	102	7.5	618	US-09-248-796A-19273	Sequence 19273, A
27	102	7.5	2090	US-09-538-092-1081	Sequence 1081, Ap

28	102	7.5	2120	US-09-949-016-9768	Sequence 9768, Ap
29	101.5	7.4	522	US-09-538-092-1096	Sequence 1096, Ap
30	100.5	7.4	195	US-09-252-991A-18814	Sequence 18814, A
31	98.5	7.2	2110	US-09-270-767-46547	Sequence 46547, A
32	98	7.2	258	US-09-248-796A-23723	Sequence 23723, A
33	97.5	7.2	970	US-09-270-767-42741	Sequence 42741, A
34	97	7.1	155	US-08-209-747-15	Sequence 15, Appl
35	97	7.1	155	US-08-458-298-15	Sequence 15, Appl
36	97	7.1	213	US-08-489-039A-11130	Sequence 11130, A
37	97	7.1	832	US-08-209-747-2	Sequence 2, Appl
38	97	7.1	832	US-08-458-298-2	Sequence 2, Appl
39	95.5	7.0	1227	US-08-448-170-8	Sequence 8, Appl
40	95.5	7.0	1227	US-08-961-803-9	Sequence 9, Appl
41	95.5	7.0	1227	US-09-661-332A-63	Sequence 63, Appl
42	95	7.0	1026	US-08-194-280-7	Sequence 7, Appl
43	95	7.0	1026	US-08-614-377A-7	Sequence 7, Appl
44	95	7.0	1026	US-09-142-648B-7	Sequence 7, Appl
45	94.5	6.9	222	US-09-545-216A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-09-598-401C-70  
Sequence 70, Application US/09598401C  
Patent No. 6596925  
GENERAL INFORMATION:  
APPLICANT: Perera, J. Ranjan  
APPLICANT: Eagleton, Clare  
TITLE OF INVENTION: Compositions and Methods for the  
TITLE OF INVENTION: Modification of Gene Expression  
FILE REFERENCE: 11000.1036C2  
CURRENT FILING DATE: US/09/598, 401C  
PRIOR FILING DATE: 2000-06-20  
PRIOR APPLICATION NUMBER: U.S. No. 6596925 60/146,591  
PRIOR FILING DATE: 1999-07-30  
PRIOR APPLICATION NUMBER: PCT/NZ00/00018  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: U.S. No. 6596925 09/276,599  
NUMBER OF SEQ ID NOS: 120  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 70  
LENGTH: 214  
TYPE: PRT  
ORGANISM: Eucalyptus grandis  
US-09-598-401C-70

Query Match 21.9%; Score 298.5; DB 4; Length 214;  
Best Local Similarity 46.0%; Pred. No. 7.4e-20;  
Matches 69; Conservative 16; Mismatches 48; Indels 17; Gaps 6;

QY 23 ISDOEQ-LPQPCDSNTKFCYNNYVFSQPRHFKCKRREYWTGTLRDVPGGCTRX 81  
DB 14 IKPQEQALKKPRCDSTYTKFCYNNYVLSQPRHFKCKRYWTKGALRVVPGGGGRK 73  
QY 82 SAKSRRTCSN-SSSSSVGVVNSNGVPLQTPVLPQS-SISNGVHTVTSDDKQSA 138  
DB 74 NKRAKRAVDHVSQONEASTSAAPGNEVP-DRSPFEPSSKSIYVG-----GEN 121  
QY 139 LSLGSPFTSLTNNNAATATHGSGSVGI 168  
DB 122 MWLTG-LPFSRIQDRAALAHGSSSFLGM 150

RESULT 2  
US-09-434-840-6  
Sequence 6, Application US/09434840  
Patent No. 6620985  
GENERAL INFORMATION:  
APPLICANT: Glazebrook, Jane

```

; APPLICANT: Jirage, Dayadevi
; APPLICANT: Toocle, Tina L
; APPLICANT: Zhou, Nan
; APPLICANT: Feys, Bart
; TITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR
; FILE REFERENCE: 043503.0009
; CURRENT APPLICATION NUMBER: US/09/434,840
; CURRENT FILING DATE: 1999-11-04
; EARLIER APPLICATION NUMBER: 09/190,733
; EARLIER FILING DATE: 1998-11-12
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-434-840-6

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Query Match 18.6%; Score 253.5; DB 4; Length 60;
Best Local Similarity 72.9%; Pred. No. 2e-16;
Matches 43; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

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QY 32 CPCRDSSTKCYNNNNYFSGPRHCKRCRYWTHGTLRPVGGGTRKAKSRICS 90
Db 2 CPCRGSSTKCYNNNSLTQPRYFCGCRRYWTKGSLRNVPGGGRKS RPKSSS 59

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RESULT 3
US-09-248-796A-14274
; Sequence 14274, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 14274
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-14274

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```

Query Match 9.5%; Score 129; DB 4; Length 712;
Best Local Similarity 26.0%; Pred. No. 0.002;
Matches 58; Conservative 27; Mismatches 60; Indels 78; Gaps 12;

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QY 89 CSNSSSSVSGV-----VSNSNGVPLQTTPLFPOSSISNGVHTTTESDGK 136
Db 459 CFESTTLVSSVPCPTQVPGVFTSTDNHGVPIASIDVTGAATVSN---TIRAQDSTG 514
QY 137 -----SALSICGSFTSTLNLN-----NAATAHSGSVYIGIGFGICGSGFPD 181
Db 515 FTSAGNAITTAITATGATTTVSGGSGSTIDYNAAGTTAAGSGDSG--SGSGSGSGSGSS 573
QY 182 VSFGI-----GRAMPFSTVGTAT-----TTNVGSN-----GG 209
Db 574 NTVGIVNPKVSSAASGITVAASASAGOS--WPYSSGSGGNGVPLPLGANNVSGNOTPTVSG 632
QY 210 HHAVPMATWQFEGLESNAGGPFVSGEYFAMPDLSTTPGSL 252
Db 633 GSNNSPTVTGAAGV-----GGVVSQS-----PSYS-----GNSL 662

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RESULT 4
US-08-808-599A-24
; Sequence 24, Application US/0808599A

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; Patent No. 6111089
; GENERAL INFORMATION:
; APPLICANT: Fukuda, Michiko N.
; TITLE OF INVENTION: Trophinin, Trophinin-Assisting
; TITLE OF INVENTION: Proteins and Methods to Inhibit Implantation
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,599A
; FILING DATE: 28-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/317,522
; FILING DATE: 04-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/439,818
; FILING DATE: 12-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LA 2256
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1160 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-808-599A-24

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```

Query Match 9.0%; Score 123; DB 3; Length 1160;
Best Local Similarity 27.6%; Pred. No. 0.014;
Matches 64; Conservative 24; Mismatches 76; Indels 68; Gaps 14;

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QY 67 GGTLRD-VPIVGGTRKSARKSRICSN-----SSSSVSGVYSNSN----- 105
Db 681 GGALNNNSAGFGAISTSPGALNNNSAGFGAISTVASFGAISNSPDEGAFSTSVGF 740
QY 106 GVPLOTT-----PVLFF-----POSSISNGVHTTTESDGKALSIC-GSFTSTL 150
Db 741 GGTLLTDFGSNHSNLSISFSAAPTTSVSGSHSTNLCFGAGASTSLCFPSASNTNL 800
QY 151 -----NHNAATATHSGSGVIGI-----GFGIGLG--SGFPD---VSFGI 192
Db 801 GSNSTNCFGATSANFEHGHISFGNGLSTVSAGFGNGLSTVSAGFDSGLSTGFGSLGP 860
QY 193 FSTVGTATTTNVNSNGHNAVPMPTWQFE-GLESNA-----GFVSG 235
Db 861 SASFNGGLGTSTGFGG-----LGTSTDFSGGNHNAHDFNGIGNSAGFNGG 907

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```

RESULT 5
US-08-317-522A-3
; Sequence 3, Application US/08317522A
; Patent No. 5599918
; GENERAL INFORMATION:
; APPLICANT: Fukuda, Michiko N.
; TITLE OF INVENTION: Trophinin and Trophinin-Assisting
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 13

```



```
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/439,818
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 2252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 674 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-751-965-3

Query Match      8.7%; Score 119; DB 2; Length 674;
Best Local Similarity 24.9%; Pred. No. 0.016;
Matches 65; Conservative 18; Mismatches 76; Indels 102; Gaps 11;

QY 67 GGT-L-RDVPVGGGTRKSA-----KRSRTCSNSSSSSVGVVSN---NGVPLQTPV 114
DB 290 GGTLLSTVCFGGSPSTSAFGGALNTNASFGCAVSTSAFSGAVSTACFSGAPI-TNPG 348
QY 115 L-----PPOSSISNGVTHVTESDGKSAALSLC-GSFTSTLLN 151
DB 349 FGCAFTSAGFGALSTADFGCTPNSIGFGAAPSTSVSFGAHGTSLCFGAAPSTSLC 408
QY 152 HNAATA-----THGSGSVIGIG-----GFG 172
DB 409 FGSAASNTNLCFGPPSTSAFSGATSPSPCDGPSTSTGFSFGNGLSTGFGGLNTSAGFG 468
QY 173 IGLG-----SGFD---DVSFGLGRAMWPSTVGTATTNTVNSGCHHAVMPA 217
DB 469 GGLGTSAGFSGGLSTSSGFDGLGTSAGFGGPGTSTGFGGLGTSAGFSGG-----520
QY 218 TWOPEGLSNAGGFGVSGEYF 238
DB 521 ----LGTSAFGGGLVTSDF 537

RESULT 8
US-08-738-975-3
Sequence 3, Application US/08738975
Patent No. 5880267
GENERAL INFORMATION:
APPLICANT: Fukuda, Michiko N.
TITLE OF INVENTION: Trophinin and Trophinin-Assisting
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/738,975
FILING DATE: herewith
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/439,818
FILING DATE: 05-Dec-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
```

```
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 2251
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 674 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-738-975-3

Query Match      8.7%; Score 119; DB 2; Length 674;
Best Local Similarity 24.9%; Pred. No. 0.016;
Matches 65; Conservative 18; Mismatches 76; Indels 102; Gaps 11;

QY 67 GGT-L-RDVPVGGGTRKSA-----KRSRTCSNSSSSSVGVVSN---NGVPLQTPV 114
DB 290 GGTLLSTVCFGGSPSTSAFGGALNTNASFGCAVSTSAFSGAVSTACFSGAPI-TNPG 348
QY 115 L-----PPOSSISNGVTHVTESDGKSAALSLC-GSFTSTLLN 151
DB 349 FGCAFTSAGFGALSTADFGCTPNSIGFGAAPSTSVSFGAHGTSLCFGAAPSTSLC 408
QY 152 HNAATA-----THGSGSVIGIG-----GFG 172
DB 409 FGSAASNTNLCFGPPSTSAFSGATSPSPCDGPSTSTGFSFGNGLSTGFGGLNTSAGFG 468
QY 173 IGLG-----SGFD---DVSFGLGRAMWPSTVGTATTNTVNSGCHHAVMPA 217
DB 469 GGLGTSAGFSGGLSTSSGFDGLGTSAGFGGPGTSTGFGGLGTSAGFSGG-----520
QY 218 TWOPEGLSNAGGFGVSGEYF 238
DB 521 ----LGTSAFGGGLVTSDF 537

RESULT 9
US-08-728-626-3
Sequence 3, Application US/08728626
Patent No. 5910451
GENERAL INFORMATION:
APPLICANT: Fukuda, Michiko N.
TITLE OF INVENTION: Trophinin and Trophinin-Assisting
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,626
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/439,818
FILING DATE: 12-MAY-1995
APPLICATION NUMBER: US 08/317,522
FILING DATE: 04-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1563
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
```



QY 67 GGTLLRDVPGVGGTRKSA-----KRSRTCSNSSSSSVGVVNS---NGVPLQTTTPV 114  
 Db 358 GGTLLSTVCFGGSPSTAGFGGALNTNNSFGCAVSTASFSGAVSTACFGAPI-TNPG 416  
 QY 115 L-----PPOSSISNGVTHVTESDGKSAISLC-GSFTSTLLN 151  
 Db 417 FGAFSTAGFGGALSTADFGGTPTNSIGFGAAPSTSVSFGGAHGTSLCFGAPSTSLC 476  
 QY 152 HNA-----ATAT-----HSGSVIGIG-----G 170  
 Db 477 FGASNTNLCFGGPPSTACTSGATSPSCDGPSTSTGFSFGNLSTNAGFGGGLNTSAG 536  
 QY 171 FGIGLG-----SGFD---DVSFGIGRAMMPPSTVGTATTNNVSGNGHHAVPM 215  
 Db 537 FCGGLGTSAGFSGGLSTSSGFDGGLGTSAGFGGPGHSTGTGFGGLGTSAGFSGSG----- 590  
 QY 216 PATWQFEGLESNAGGFGVSGEYF 238  
 Db 591 -----LGTSAFGGGLVTSDF 607

## RESULT 12

US-08-439-818A-2  
 ; Sequence 2, Application US/08439818A  
 ; Patent No. 5654145  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fukuda, Michiko N.  
 ; TITLE OF INVENTION: Trophinin and Trophinin-Assisting  
 ; TITLE OF INVENTION: Proteins  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Campbell and Flores  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/439, 818A  
 ; FILING DATE: 12-MAY-1995  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/317,522  
 ; FILING DATE: 04-OCT-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Campbell, Cathryn A.  
 ; REGISTRATION NUMBER: 31,815  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 535-9001  
 ; TELEFAX: (619) 535-8949  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 749 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-439-818A-2

Query Match 8.3%; Score 113; DB 1; Length 749;

Best Local Similarity 25.1%; Pred. No. 0.066; Mismatches 74; Indels 104; Gaps 12;

QY 67 GGTLLRDVPGVGGTRKSA-----KRSRTCSNSSSSSVGVVNS---NGVPLQTTTPV 114  
 Db 358 GGTLLSTVCFGGSPSTAGFGGALNTNNSFGCAVSTASFSGAVSTACFGAPI-TNPG 416

QY 115 L-----PPOSSISNGVTHVTESDGKSAISLC-GSFTSTLLN 151  
 Db 417 FGAFSTAGFGGALSTADFGGTPTNSIGFGAAPSTSVSFGGAHGTSLCFGAPSTSLC 476  
 QY 152 HNA-----ATAT-----HSGSVIGIG-----G 170  
 Db 477 FGASNTNLCFGGPPSTACTSGATSPSCDGPSTSTGFSFGNLSTNAGFGGGLNTSAG 536  
 QY 171 FGIGLG-----SGFD---DVSFGIGRAMMPPSTVGTATTNNVSGNGHHAVPM 215  
 Db 537 FCGGLGTSAGFSGGLSTSSGFDGGLGTSAGFGGPGHSTGTGFGGLGTSAGFSGSG----- 590  
 QY 216 PATWQFEGLESNAGGFGVSGEYF 238  
 Db 591 -----LGTSAFGGGLVTSDF 607

## RESULT 13

US-08-751-965-2  
 ; Sequence 2, Application US/08751965  
 ; Patent No. 5858360  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Fukuda, Michiko N.  
 ; TITLE OF INVENTION: Trophinin and Trophinin-Assisting  
 ; TITLE OF INVENTION: Proteins  
 ; NUMBER OF SEQUENCES: 22  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Campbell and Flores  
 ; STREET: 4370 La Jolla Village Drive, Suite 700  
 ; CITY: San Diego  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 92122  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/751,965  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/439,818  
 ; FILING DATE: 12-MAY-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Campbell, Cathryn A.  
 ; REGISTRATION NUMBER: 31,815  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (619) 535-9001  
 ; TELEFAX: (619) 535-8949  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 749 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-751-965-2

Query Match 8.3%; Score 113; DB 2; Length 749;

Best Local Similarity 25.1%; Pred. No. 0.066; Mismatches 74; Indels 104; Gaps 12;

QY 67 GGTLLRDVPGVGGTRKSA-----KRSRTCSNSSSSSVGVVNS---NGVPLQTTTPV 114  
 Db 358 GGTLLSTVCFGGSPSTAGFGGALNTNNSFGCAVSTASFSGAVSTACFGAPI-TNPG 416  
 QY 115 L-----PPOSSISNGVTHVTESDGKSAISLC-GSFTSTLLN 151  
 Db 417 FGAFSTAGFGGALSTADFGGTPTNSIGFGAAPSTSVSFGGAHGTSLCFGAPSTSLC 476  
 QY 152 HNA-----ATAT-----HSGSVIGIG-----G 170

[illegible]

RESULT 14  
US-08-738-975-2  
; Sequence 2, Application US/08738975

```

1      GENERAL INFORMATION:
2      APPLICANT: Fukuda, Michiko N.
3      TITLE OF INVENTION: Trophinin and Trophinin-Assisting
4      TITLE OF INVENTION: Proteins
5      NUMBER OF SEQUENCES: 22
6      CORRESPONDENCE ADDRESS:
7      ADDRESSEE: Campbell and Flores
8      STREET: 4370 La Jolla Village Drive, Suite 700
9      CITY: San Diego
10     STATE: California
11     COUNTRY: USA
12     ZIP: 92122
13
14     COMPUTER READABLE FORM:
15     MEDIUM TYPE: Floppy disk
16     COMPUTER: IBM PC compatible
17     OPERATING SYSTEM: PC-DOS/MS-DOS
18     SOFTWARE: PatentIn Release #1.0, Version #1.25
19
20     CURRENT APPLICATION DATA:
21     APPLICATION NUMBER: US/08/738,975
22     FILING DATE: herewith
23     CLASSIFICATION: 435
24     PRIOR APPLICATION DATA:
25     APPLICATION NUMBER: US 08/439,818
26     FILING DATE: 05-Dec-1995
27
28     ATTORNEY/AGENT INFORMATION:
29     NAME: Campbell, Cathryn A.
30     REGISTRATION NUMBER: 31,815
31     REFERENCE/DOCKET NUMBER: P-LA 2251
32     TELECOMMUNICATION INFORMATION:
33     TELEPHONE: (619) 535-9001
34     TELEFAX: (619) 535-8949
35
36     INFORMATION FOR SEQ ID NO: 2:
37     SEQUENCE CHARACTERISTICS:
38     LENGTH: 749 amino acids
39     TYPE: amino acid
40     TOPOLOGY: linear
41
42     MOLECULE TYPE: protein
43
44     US-08-738-975-2

```

Query Match	8.3%	Score 113;	DB 2;	Length 749;
Best Local Similarity	25.1%;	Pred. No. 0.066;		
Matches	66;	Conservative	19;	Mismatches 74;
				Indels 104;
				Gaps 12

```

Qy 67 GGT-ADPEVGGGTRSA-----KSRFTCSNSSSSVGGVYNS---NGVDLOTPV 114
Db 358 GGLTSTSVCFGGSPTSSAGFGALNTMNSFGCAVSTSAISFGAVSTACRSAP I -TNP G 416
Qy 115 L-----PQSSISNGVTHITTESDQKSAISLC-GSETFTLLN 151
Db 417 FCGAFSTSAFCGALSTADFCGTPTSNISFGAAPSTSVISFGAGHTSLCFGAPSTSLC 476
Qy 152 HNNA-----ATAT-----HSGSGVIGIG-----G 170
Db 477 FGSASNTNLCPFSGPSTACFSFGATSPRCDFGSPSTISITFCFGNLSTNAGGGGALNTSAG 536
Qy 171 FGLGLG-----SGFD---DVSPGLGRAMPSTVGTATTTNVGNSNGGHAIVFM 215

```

```

Db      537  FGGGLTSGTSGFGGGLTSSGFGDGLGTSGAGFGGGPSTGRGGGLTSGAGSGG----- 590
Qy      216  PATWPEGLAESNAGGFPVSGEYF 238
          | : ||| | : |
Db      591  -----LGTSGAGGGGLVTSDFG 607

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RESULT 15  
US-08-728-626-2  
; Sequence 2, Application US/08728626

```

1  GENERAL INFORMATION:
2  APPLICANT: Fukuda, Michio N.
3  TITLE OF INVENTION: Trophinin and Trophinin-Assisting
4  TITLE OF INVENTION: Proteins
5  NUMBER OF SEQUENCES: 22
6  CORRESPONDENCE ADDRESS:
7  ADDRESSEE: Campbell and Flores
8  STREET: 4370 La Jolla Village Drive, Suite 700
9  CITY: San Diego
10 STATE: California
11 COUNTRY: USA
12 ZIP: 92122
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Patent In Release #1.0, Version #1.25
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/728,626
21 FILING DATE:
22 CLASSIFICATION: 435
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: US 08/439,818
25 FILING DATE: 12-MAY-1995
26 APPLICATION NUMBER: US 08/317,522
27 FILING DATE: 04-OCT-1994
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Campbell, Cathryn A.
30 REGISTRATION NUMBER: 31,815
31 REFERENCE/DOCKET NUMBER: P-LA 1563
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (619) 535-9001
34 TELEFAX: (619) 535-8949
35 INFORMATION FOR SEQ ID NO: 2:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 749 amino acids
38 TYPE: amino acid
39 TOPOLOGY: linear
40 MOLECULE TYPE: protein
41
42 US-08-728-626-2

```

Query Match	8.3%;	Score 113;	DB 2;	Length 749;
Best Local Similarity	25.1%;	Pred. No. 0.066;		
Matches	66;	Conservative	19;	Mismatches 74;
				Indels 104;
				Gaps 12

QY	67	GGGT--RDVYGGGCTKSA-----KSRFTCSNSSSSSVGYVSN---NGVPLQTPV	114
Db	358	GGTLSTVCFGGSPBSTSAGFGGALNTNNAFCGCAVSTASPSGAVSTACSAGPI--TNPG	416
QY	115	L-----PPOSSISNGVHTVTEBDKGKASLSC-GSFTSTLNN	151
Db	417	FGGAFSTAGFCGALSTAADFCGFTPSNLSIGGAAPSTSVSPCGAHGTLSCFGGAPSTSLC	476
QY	152	HMAA-----ATAT-----HGSGSVIGIG-----G	170
Db	477	FGSAANTNLFCGGPPSTSAFCGATSPBFCDBPSTSTGSPFGNGLSTNAGFCGGGLNTSAG	536
QY	171	FGIGLG-----SGFD--DVSFGGLGRMAFPSTVGTATTTNVGNSNGHNAVPM	215
Db	537	FGGGLGTAGSPGCGSLSTSSGFDGGLGTSAGRCGGSPGRTSTFGGGLGTSAGFSGG-----	590
QY	216	PAITWQEGLESNAGGAFVSGEYF	238

Db 591 -----|: ||| |: |  
-LGTSAFGGGLVTSDDF 607

Search completed: November 3, 2005, 16:14:33  
Job time : 45 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 3, 2005, 16:11:06 ; Search time 167 Seconds  
(without alignments)  
633.878 Million cell updates/sec

Title: US-10-509-691-2  
Perfect score: 133  
Sequence: 1 MPTSDGEPRIAMKNGVT.....SGEYFAMPDLITTPGNSLK 253

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA.\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*  
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8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
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18: /cgn2\_6/ptodata/1/pubpaa/US10A\_NEW\_PUB.pep.\*  
19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*  
21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	651	47.8	225	US-10-225-066A-128	Sequence 128, App
2	651	47.8	225	US-10-225-067-6	Sequence 6, App1
3	651	47.8	225	US-10-374-780A-2760	Sequence 2760, App
4	651	47.8	225	US-10-225-066A-128	Sequence 128, App
5	436.5	33.0	156	US-10-424-599-268677	Sequence 268677, App
6	402	29.5	209	US-10-225-066A-404	Sequence 404, App
7	402	29.5	209	US-10-374-780A-2762	Sequence 2762, App
8	402	29.5	209	US-10-225-066A-404	Sequence 404, App
9	377.5	27.7	204	US-10-225-066A-406	Sequence 406, App
10	377.5	27.7	204	US-10-374-780A-362	Sequence 362, App
11	377.5	27.7	204	US-10-225-066A-406	Sequence 406, App

12	377.5	27.7	206	15	US-10-425-114-40748	Sequence 40748, A
13	376.5	27.6	211	15	US-10-424-599-187121	Sequence 187121, A
14	376.5	27.6	211	15	US-10-425-114-43084	Sequence 43084, A
15	356	26.1	211	15	US-10-424-599-239234	Sequence 239234, A
16	355	26.0	211	15	US-10-424-599-239232	Sequence 239232, A
17	352	25.8	383	16	US-10-425-115-205283	Sequence 205283, A
18	341	25.0	401	15	US-10-425-114-46978	Sequence 46978, A
19	335	24.6	300	15	US-10-424-599-219343	Sequence 219343, A
20	335	24.6	324	15	US-10-424-599-218016	Sequence 218016, A
21	335	24.6	329	15	US-10-425-114-37734	Sequence 37734, A
22	335	24.6	352	15	US-10-425-114-56857	Sequence 56857, A
23	334	24.5	220	16	US-10-437-963-193177	Sequence 193177, A
24	333.5	24.5	339	15	US-10-425-114-42241	Sequence 42241, A
25	333.5	24.5	339	15	US-10-425-114-53358	Sequence 53358, A
26	333.5	24.5	341	15	US-10-424-599-200270	Sequence 200270, A
27	331	24.3	378	15	US-10-425-114-57083	Sequence 57083, A
28	331	24.3	378	16	US-10-425-115-199078	Sequence 199078, A
29	330.5	24.2	344	16	US-10-425-115-298984	Sequence 298984, A
30	330.5	24.2	275	15	US-10-425-114-53945	Sequence 63945, A
31	328	24.1	389	16	US-10-437-963-162230	Sequence 162230, A
32	328	24.1	452	16	US-10-437-963-162233	Sequence 162233, A
33	327	24.0	328	16	US-10-425-115-259592	Sequence 259592, A
34	327	24.0	330	15	US-10-425-114-37762	Sequence 37762, A
35	326	23.9	329	15	US-10-425-114-38607	Sequence 38607, A
36	326	23.9	348	15	US-10-424-599-199578	Sequence 199578, A
37	325.5	23.9	375	16	US-10-437-963-117427	Sequence 117427, A
38	325	23.8	333	15	US-10-425-114-57014	Sequence 57014, A
39	325	23.8	352	16	US-10-425-115-191735	Sequence 191735, A
40	325	23.8	347	16	US-10-425-115-204367	Sequence 204367, A
41	323	23.7	348	16	US-10-437-963-124974	Sequence 124974, A
42	323	23.7	360	16	US-10-425-115-342526	Sequence 342526, A
43	322.5	23.7	360	16	US-10-739-930-13883	Sequence 7383, App
44	322	23.6	371	16	US-10-437-963-124876	Sequence 124976, A
45	321.5	23.6	355	16	US-10-437-963-191965	Sequence 191965, A

## ALIGNMENTS

RESULT 1  
US-10-225-066A-128  
; Sequence 128, Application US/10225066A  
; Publication No. US20030226173A1  
GENERAL INFORMATION:  
; APPLICANT: Mendel Biotechnology, Inc.  
; APPLICANT: RATCLIFFE, Oliver  
; APPLICANT: RIECHMANN, Jose Luis  
; APPLICANT: ADAM, Luc J  
; APPLICANT: DUBELL, Arnold T  
; APPLICANT: HEARD, Jacqueline E  
; APPLICANT: PILGRIM, Marsha L  
; APPLICANT: JIANG, Cai-Zhong  
; APPLICANT: REUBER, T. Lynne  
; APPLICANT: CREELMAN, Robert A  
; APPLICANT: PINEDA, Omeira  
; APPLICANT: YU, Guo-Liang  
; APPLICANT: BROWN, Pierre E  
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants  
; FILE REFERENCE: ME10036-2 US  
; CURRENT APPLICATION NUMBER: US/10/225,066A  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: 09/837,444  
; PRIOR FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: 60/310,847  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 60/336,049  
; PRIOR FILING DATE: 2001-12-05  
; PRIOR APPLICATION NUMBER: 60/338,692  
; PRIOR FILING DATE: 2001-12-11  
; PRIOR APPLICATION NUMBER: 10/171,468  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 1122  
; SOFTWARE: PatentIn version 3.1

SEQ ID NO 128  
LENGTH: 225  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-10-225-066A-128

Query Match 47.8%; Score 651; DB 15; length 225;  
Best Local Similarity 55.5%; Pred. No. 8.5e-52;  
Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;

OY 1 MPTSDSGEPRIAMKPNK-----VTVPISDQEQQLPCPRCDSNTKFCYNNYNFSQPRHF 56  
Db 1 MP-SSEFSRRVPKIPHGQGSVAIP-TDQOEQLSCPRCSTNTKFCYNNYNFSQPRHF 58  
OY 57 CKACRRYWTGGTLRDVPGGTRKSAKRRTCSNSSSVGVNSNGVPLQTPPLVF 116  
Db 59 CKSCRRTYTHGGTLRDVPGGTRKSAKRRTCSNSSSVGVNSNGVPLQTPPLVF 114  
OY 117 POSSISNGVTHVTYESDGKSAISLCSGFTSTLLNHNAAATATHGSGSVIGIGFGIGLG 176  
Db 115 POSSISNGGIT-----TAKGSASFFYGGF-SSLINYNAAVRNPGGFGNPGDAFGLGLG 167  
OY 177 SG--FDVVSFGLGRAMPFSTVGT--ATTNVGSGHGAHPMPATWQFEGLESNAGGF 232  
Db 168 HGSYYEDVRYGQGITVWPFSSGATDAATTS-----HIAQIPATWQFEGQESKV--GF 218  
OY 233 VSGEYFA 239  
Db 219 VSGDYVA 225

## RESULT 2

US-10-225-067-6  
Sequence 6, Application US/10225067  
Publication No. US20040019925A1  
GENERAL INFORMATION:  
APPLICANT: Mendel Biotechnology, Inc.  
APPLICANT: Heard, Jacqueline E.  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Creelman, Robert A.  
APPLICANT: Keddie, James  
APPLICANT: Pilgrim, Martha L.  
APPLICANT: Dubell, Arnold T.  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Pineda, Omalra  
APPLICANT: Yu, Guo-Liang  
APPLICANT: Broun, Pierre E.  
TITLE OF INVENTION: BIOCHEMISTRY-RELATED POLYNUCLEOTIDES AND  
FILE REFERENCE: 51442002042  
CURRENT APPLICATION NUMBER: US/10/225,067  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 60/310,847  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 60/336,049  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/338,692  
PRIOR FILING DATE: 2001-12-11  
PRIOR APPLICATION NUMBER: 10/171,468  
PRIOR FILING DATE: 2002-06-14  
NUMBER OF SEQ ID NOS: 148  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 225  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
FEATURE:  
NAME/KEY: DOMAIN  
LOCATION: (34)...(62)  
OTHER INFORMATION: Conserved domain  
US-10-225-067-6

Query Match 47.8%; Score 651; DB 15; length 225;  
Best Local Similarity 55.5%; Pred. No. 8.5e-52;  
Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;

OY 1 MPTSDSGEPRIAMKPNK-----VTVPISDQEQQLPCPRCDSNTKFCYNNYNFSQPRHF 56  
Db 1 MP-SSEFSRRVPKIPHGQGSVAIP-TDQOEQLSCPRCSTNTKFCYNNYNFSQPRHF 58  
OY 57 CKACRRYWTGGTLRDVPGGTRKSAKRRTCSNSSSVGVNSNGVPLQTPPLVF 116  
Db 59 CKSCRRTYTHGGTLRDVPGGTRKSAKRRTCSNSSSVGVNSNGVPLQTPPLVF 114  
OY 117 POSSISNGVTHVTYESDGKSAISLCSGFTSTLLNHNAAATATHGSGSVIGIGFGIGLG 176  
Db 115 POSSISNGGIT-----TAKGSASFFYGGF-SSLINYNAAVRNPGGFGNPGDAFGLGLG 167  
OY 177 SG--FDVVSFGLGRAMPFSTVGT--ATTNVGSGHGAHPMPATWQFEGLESNAGGF 232  
Db 168 HGSYYEDVRYGQGITVWPFSSGATDAATTS-----HIAQIPATWQFEGQESKV--GF 218  
OY 233 VSGEYFA 239  
Db 219 VSGDYVA 225

## RESULT 3

US-10-374-780A-2760  
Sequence 2760, Application US/10374780A  
Publication No. US20040019927A1  
GENERAL INFORMATION:  
APPLICANT: Sherman, Bradley K.  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: Jiang, Cai-Zhong  
APPLICANT: Heard, Jacqueline E.  
APPLICANT: Haake, Volker  
APPLICANT: Creelman, Robert A.  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: Reuber, T. Lynne  
APPLICANT: Keddie, James  
APPLICANT: Broun, Pierre E.  
APPLICANT: Pilgrim, Martha L.  
APPLICANT: Dubell III, Arnold T.  
APPLICANT: Pineda, Omalra  
APPLICANT: Yu, Guo-Liang  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS  
FILE REFERENCE: MBI-0047 CIP  
CURRENT APPLICATION NUMBER: US/10/374,780A  
PRIOR FILING DATE: 2003-02-25  
PRIOR APPLICATION NUMBER: 09/837,944  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: 60/310,847  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/934,455  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/336,049  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/338,692  
PRIOR FILING DATE: 2001-12-11  
PRIOR APPLICATION NUMBER: 10/171,468  
PRIOR FILING DATE: 2002-06-14  
PRIOR APPLICATION NUMBER: 10/225,066  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/225,067  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 10/225,068  
PRIOR FILING DATE: 2002-08-09  
NUMBER OF SEQ ID NOS: 2906  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2760  
LENGTH: 225  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana

FEATURE:  
OTHER INFORMATION: G1897  
US-10-374-780A-2760

Query Match 47.8%; Score 651; DB 15; Length 225;  
Best Local Similarity 55.5%; Pred. No. 8.5e-52;  
Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;

QY 1 MPTSDSGEPRIAMKPNP-----VTVPISDQEQOLPCPCDSSNTKFCYNNYNNFSQPRHF 56  
DB 1 MP-SEFSSRRVPKIPHGQGSVAIP-TDQEQQLSCPCESNTKFCYNNYNNFSQPRHF 58  
QY 57 CKACRRYTHGTLRDVPVGGGTRKSAKRSRTCSNSSSVSGVNSNGVPLQTPVLF 116  
DB 59 CKSCRRTYTHGTLRDIPVGGVSRKSKRSRTYSSAATTSYVG-----SRNPPLQATPVLF 114  
QY 117 POSSISNGVTHTVTESDQKGSALSLCGSFTSTLNNHNAATAATHGSGSVIGIGGIGLG 176  
DB 115 POSSISNGIT-----TAKGSASSFYGGF-SLLIYNNAVSRNPGGPGFNGPDAGLGLG 167  
QY 177 SG--FDDVSFGLGRAMPFSTVGT--ATTNVGSGHGAHPMPATWQFEGLESNAGGAF 232  
DB 168 HGSYEDRVYQGITWPFSSGATDAATTS-----HIAQIPATWQFEGQESKV--GF 218  
QY 233 VSGEYFA 239  
DB 219 VSGDYVA 225

#### RESULT 4

US-10-225-066A-128  
Sequence 128, Application US/10225066A  
Publication No. US20050160493A9  
GENERAL INFORMATION:  
APPLICANT: Mendel Biotechnology, Inc.  
APPLICANT: RATCLIFFE, Oliver  
APPLICANT: RIECHMANN, Jose Luis  
APPLICANT: ADAM, Luc J  
APPLICANT: DUBBEL, Arnold T  
APPLICANT: HEARD, Jacqueline E  
APPLICANT: PILGRIM, Marsha L  
APPLICANT: JIANG, Cai-Zhong  
APPLICANT: REUBER, T. Lynne  
APPLICANT: CREELMAN, Robert A  
APPLICANT: PINEDA, Omaira  
APPLICANT: YU, Guo-Liang  
APPLICANT: BROUN, Pierre E  
TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants  
FILE REFERENCE: MB10036-2 US  
CURRENT APPLICATION NUMBER: US/10/225,066A  
CURRENT FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 09/837,444  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: 60/310,847  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 60/336,049  
PRIOR FILING DATE: 2001-12-05  
PRIOR APPLICATION NUMBER: 60/338,692  
PRIOR FILING DATE: 2001-12-11  
PRIOR APPLICATION NUMBER: 10/171,468  
PRIOR FILING DATE: 2002-06-14  
NUMBER OF SEQ ID NOS: 1122  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 128  
LENGTH: 225  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-10-225-066A-128

Query Match 47.8%; Score 651; DB 18; Length 225;  
Best Local Similarity 55.5%; Pred. No. 8.5e-52;  
Matches 137; Conservative 31; Mismatches 49; Indels 30; Gaps 10;

QY 1 MPTSDSGEPRIAMKPNP-----VTVPISDQEQOLPCPCDSSNTKFCYNNYNNFSQPRHF 56  
DB 1 MP-SEFSSRRVPKIPHGQGSVAIP-TDQEQQLSCPCESNTKFCYNNYNNFSQPRHF 58  
QY 57 CKACRRYTHGTLRDVPVGGGTRKSAKRSRTCSNSSSVSGVNSNGVPLQTPVLF 116  
DB 59 CKSCRRTYTHGTLRDIPVGGVSRKSKRSRTYSSAATTSYVG-----SRNPPLQATPVLF 114  
QY 117 POSSISNGVTHTVTESDQKGSALSLCGSFTSTLNNHNAATAATHGSGSVIGIGGIGLG 176  
DB 115 POSSISNGIT-----TAKGSASSFYGGF-SLLIYNNAVSRNPGGPGFNGPDAGLGLG 167  
QY 177 SG--FDDVSFGLGRAMPFSTVGT--ATTNVGSGHGAHPMPATWQFEGLESNAGGAF 232  
DB 168 HGSYEDRVYQGITWPFSSGATDAATTS-----HIAQIPATWQFEGQESKV--GF 218  
QY 233 VSGEYFA 239  
DB 219 VSGDYVA 225

#### RESULT 5

US-10-424-599-268677  
Sequence 268677, Application US/10424599  
Publication No. US20040031072A1  
GENERAL INFORMATION:  
APPLICANT: La Rosa Thomas J  
APPLICANT: KOVALLIC David K  
APPLICANT: Zhou Yihua  
APPLICANT: Cao Yongwei  
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
FILE REFERENCE: 38-21(53223)B  
CURRENT APPLICATION NUMBER: US/10/424,599  
CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684  
SEQ ID NO 268677  
LENGTH: 156  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_84638C.1.pep  
US-10-424-599-268677

Query Match 32.0%; Score 436.5; DB 15; Length 156;  
Best Local Similarity 55.1%; Pred. No. 3.7e-32;  
Matches 92; Conservative 22; Mismatches 38; Indels 15; Gaps 6;

QY 1 MPTSDSGEPRIAMKP--NGVTVPISDQEQOLPCPCDSSNTKFCYNNYNNFSQPRHFCK 58  
DB 1 MPSSNSGESRR-ASKPQSSGGAADPPPEQENPPCPCDSTVTKFCYNNYNNFSQPRHFCK 59  
QY 59 ACRRTYTHGTLRDVPVGGGTRKSAKRSRT--CNSNSSSVSGVNSNGVPLQTPVLF 116  
DB 60 SCRRTYTHGTLRDIPVGGGSRKAKRSRTTHVAATSSSSSTCMTSAQEHART--LLA 117  
QY 117 POSSISNGVTHTVTESDQKGSALSLCGSFTSTLNNHNAATAATHGSG 163  
DB 118 PVASTHYGVLDGVKQTSNGG--NVCGSFTSLNN-----TRGSG 156

#### RESULT 6

US-10-225-066A-404  
Sequence 404, Application US/10225066A  
Publication No. US20030226173A1  
GENERAL INFORMATION:  
APPLICANT: Mendel Biotechnology, Inc.  
APPLICANT: RATCLIFFE, Oliver  
APPLICANT: RIECHMANN, Jose Luis  
APPLICANT: ADAM, Luc J  
APPLICANT: DUBBEL, Arnold T  
APPLICANT: HEARD, Jacqueline E  
APPLICANT: PILGRIM, Marsha L

```
APPLICANT: JIANG, Cai-Zhong
APPLICANT: REUBER, T. Lynne
APPLICANT: CREELMAN, Robert A
APPLICANT: PINEDA, Omalra
APPLICANT: YU, Guo-Liang
APPLICANT: BROUN, Pierre E
TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
FILE REFERENCE: MB10036-2 US
CURRENT APPLICATION NUMBER: US/10/225,066A
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 09/837,444
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 1122
SOFTWARE: PatentIn version 3.1
SEQ ID NO 404
LENGTH: 209
TYPE: PR1
ORGANISM: Arabidopsis thaliana
US-10-225-066A-404
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Query Match      29.5%; Score 402; DB 15; Length 209;
Best Local Similarity 39.0%; Pred. No. 8.3e-29;
Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;
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D 1 MP-SEPNOTRPTKQFSTAAPPPNLAEPPLCPKCNSTTKFCYNNYNLAOPRYCKSC 59
QY 61 RRYWTHGTLRDVPGGGTRK-SAKRSRTCSN--SSSSSVGSVNSNGVPLQTPVLPF 117
D 60 RRYWTHGTLRDVPGGGTRSSSKRHRSFSTATSSSSSVITTTQBPATTEA---S 116
QY 118 QSSISNGVTHVTESDQKGSALSLCGSFTSTLLNHNAAATATGSGSVIGG--FGIGL 175
D 117 QTKVTNLIS-----GHGSFASLIGL-----GSGN---GGIDYGFY 149
QY 176 GSGFDVSVFG-IGRAMPFSTVGTATTNNVSGNGHHAVMPATWQFEGLESNAGGFFVS 234
D 150 GYGLEMSIGYLD-----SSVGEIPV--VDGCGD-----TWQIGETIGKSG----- 190
QY 235 GEYFAMPDLSTTPGNSLK 253
D 191 GDSLIMPGLEISMQTNDVK 209
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RESULT 7  
US-10-374-780A-2762  
Sequence 2762, Application US/10374780A  
Publication No. US2004001927A1  
GENERAL INFORMATION:

```
APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: JIANG, Cai-Zhong
APPLICANT: Heard, Jacqueline E
APPLICANT: Haake, Volker
APPLICANT: Creelman, Robert A
APPLICANT: Ratcliffe, Oliver
APPLICANT: Adam, Luc J
APPLICANT: Reuber, T. Lynne
APPLICANT: Keddie, James
APPLICANT: Broun, Pierre E
APPLICANT: Pilgrim, Marsha L
APPLICANT: Dubell IT, Arnold T
APPLICANT: Pineda, Omalra
APPLICANT: YU, Guo-Liang
```

```
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MB1-0047 CIP
CURRENT APPLICATION NUMBER: US/10/374,780A
CURRENT FILING DATE: 2003-02-25
PRIOR APPLICATION NUMBER: 09/837,944
PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/934,455
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 10/225,066
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,067
PRIOR FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 10/225,068
PRIOR FILING DATE: 2002-08-09
NUMBER OF SEQ ID NOS: 2906
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2762
LENGTH: 209
TYPE: PR1
ORGANISM: Arabidopsis thaliana
FEATURE:
OTHER INFORMATION: G1898
US-10-374-780A-2762
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Query Match      29.5%; Score 402; DB 15; Length 209;
Best Local Similarity 39.0%; Pred. No. 8.3e-29;
Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;
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QY 1 MPTSDSGEPRIAMKPNQVTPISDQOQLPCPCDSSNTKFCYNNYNFSGPRHFKAC 60
D 1 MP-SEPNOTRPTKQFSTAAPPPNLAEPPLCPKCNSTTKFCYNNYNLAOPRYCKSC 59
QY 61 RRYWTHGTLRDVPGGGTRK-SAKRSRTCSN--SSSSSVGSVNSNGVPLQTPVLPF 117
D 60 RRYWTHGTLRDVPGGGTRSSSKRHRSFSTATSSSSSVITTTQBPATTEA---S 116
QY 118 QSSISNGVTHVTESDQKGSALSLCGSFTSTLLNHNAAATATGSGSVIGG--FGIGL 175
D 117 QTKVTNLIS-----GHGSFASLIGL-----GSGN---GGIDYGFY 149
QY 176 GSGFDVSVFG-IGRAMPFSTVGTATTNNVSGNGHHAVMPATWQFEGLESNAGGFFVS 234
D 150 GYGLEMSIGYLD-----SSVGEIPV--VDGCGD-----TWQIGETIGKSG----- 190
QY 235 GEYFAMPDLSTTPGNSLK 253
D 191 GDSLIMPGLEISMQTNDVK 209
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RESULT 8  
US-10-225-066A-404  
Sequence 404, Application US/10225066A  
Publication No. US2005016049A9  
GENERAL INFORMATION:

```
APPLICANT: Mendel Biotechnology, Inc.
APPLICANT: RATCLIFFE, Oliver
APPLICANT: RIECHMANN, Jose Luis
APPLICANT: ADAM, Luc J
APPLICANT: DUBELL, Arnold T
APPLICANT: HEARD, Jacqueline E
APPLICANT: PILGRIM, Marsha L
APPLICANT: JIANG, Cai-Zhong
APPLICANT: REUBER, T. Lynne
APPLICANT: CREELMAN, Robert A
APPLICANT: PINEDA, Omalra
```

APPLICANT: YU, Guo-Liang  
APPLICANT: BROUN, Pierre E  
TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants  
FILE REFERENCE: MBI0036-2 US  
CURRENT APPLICATION NUMBER: US/10/225,066A  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 09/837,444  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: 60/310,847  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 60/336,049  
PRIOR FILING DATE: 2001-12-05  
PRIOR APPLICATION NUMBER: 60/338,692  
PRIOR FILING DATE: 2001-12-11  
PRIOR APPLICATION NUMBER: 10/171,468  
PRIOR FILING DATE: 2002-06-14  
NUMBER OF SEQ ID NOS: 1122  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 404  
LENGTH: 209  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-10-225-066A-404

Query Match 29.5%; Score 402; DB 18; Length 209;  
Best Local Similarity 39.0%; Pred. No. 8.3e-29;  
Matches 101; Conservative 35; Mismatches 67; Indels 56; Gaps 13;

QY 1 MPTSDSGPRRIAMKPNVTVPISDQOLPCPRCDSSNTKFCYNNYNSOPRHCKAC 60  
DB 1 MP-SEPNTRRPVRVQSTAAVPPVLAEPPLPCPRCNSITTKFCYNNYNNLQPRYCKSC 59  
QY 61 RRYTHGGTLRDVPGGTRK-SAKRSRTCSN--SSSSSVGSVNSNGVPLQTTVPVLP 117  
DB 60 RRYWTGGTLRDVPGGTRSSRRRSFSTTATSSSSSVITTTQEPATTEA---S 116  
QY 118 QSSISNGVTHVTESDGSALSLCGSFTSTLLNNAATATHGSGVIGIG--FGIGL 175  
DB 117 QTKYTNLIS-----GHGSFASLIGL-----GSGN---GGLDYGFXY 149  
QY 176 GSGFDVVSFG-LGRAMPFSTVGTATTNVGSGNGHAAVMPATNQFGLSMAAGGFVS 234  
DB 150 GYGLEMSIGYIGD-----SSVGEIPV--VDGCGD-----TWQIGIEKSG----- 190  
QY 235 GEYFAMPDLSTTPGNSLK 253  
DB 191 GDSLWPGLEISMOTNDVK 209

## RESULT 9

US-10-225-066A-406  
Sequence 406, Application US/10225066A  
Publication No. US20030226173A1  
GENERAL INFORMATION:  
APPLICANT: Mendel Biotechnology, Inc.  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: RICHMANN, Jose Luis  
APPLICANT: ADAM, Luc J  
APPLICANT: DUBELL, Arnold T  
APPLICANT: HEARD, Jacqueline E  
APPLICANT: PILGRIM, Marsha L  
APPLICANT: JIANG, Cai-Zhong  
APPLICANT: REUBER, T. Lynne  
APPLICANT: CREELMAN, Robert A  
APPLICANT: PINEDA, Omalta  
APPLICANT: YU, Guo-Liang  
APPLICANT: BROUN, Pierre E  
TITLE OF INVENTION: Yield-Related Polynucleotides and polypeptides in Plants  
FILE REFERENCE: MBI0036-2 US  
CURRENT APPLICATION NUMBER: US/10/225,066A  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 09/837,444  
PRIOR FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: 60/310,847  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 60/336,049  
PRIOR FILING DATE: 2001-12-05  
PRIOR APPLICATION NUMBER: 60/338,692  
PRIOR FILING DATE: 2001-12-11  
PRIOR APPLICATION NUMBER: 10/171,468  
PRIOR FILING DATE: 2002-06-14  
NUMBER OF SEQ ID NOS: 1122  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 406  
LENGTH: 204  
TYPE: PRT  
ORGANISM: Arabidopsis thaliana  
US-10-225-066A-406

Query Match 27.7%; Score 377.5; DB 15; Length 204;  
Best Local Similarity 48.8%; Pred. No. 1.5e-26;  
Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;

QY 26 QOELPCPRCDSSNTKFCYNNYNSOPRHCKACRRYTHGGTLRDVPGGTRKSAKR 85  
DB 25 EOELKCPRCDSPTKFCYNNYNNLSOPRHCKSCRRYTHGGALRNVPVGGSRKNAKTK 84  
QY 86 SRTCSNSSSVGSVNSNGVPLQTTVPVLPQSSISNGVTHT-----VTESDGSKSA 138  
DB 85 RSTSSSSASPSN--SSQNKTKAPDPDPDPKRSQKDLPTKMLYGFPGDDVYK-- 140  
QY 139 LSLGFTSTLLNNAATATHGSGVIGIGFGLG--GSGFDVVSFGLG 187  
DB 141 MEIGSFSLIANN-----MQLGLGGGIMLDGSGMDHGMGLG 179

## RESULT 10

US-10-374-780A-362  
Sequence 362, Application US/10374780A  
Publication No. US2004001927A1  
GENERAL INFORMATION:  
APPLICANT: Sherman, Bradley K  
APPLICANT: Riechmann, Jose Luis  
APPLICANT: JIANG, Cai-Zhong  
APPLICANT: HEARD, Jacqueline E  
APPLICANT: HAAKE, Volker  
APPLICANT: CREELMAN, Robert A  
APPLICANT: Ratcliffe, Oliver  
APPLICANT: ADAM, Luc J  
APPLICANT: REUBER, T. Lynne  
APPLICANT: KEDDIE, James  
APPLICANT: BROUN, Pierre E  
APPLICANT: PILGRIM, Marsha L  
APPLICANT: DUBELL III, Arnold T  
APPLICANT: PINEDA, Omalta  
APPLICANT: YU, Guo-Liang  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS  
FILE REFERENCE: MBI-0047 CIP  
CURRENT APPLICATION NUMBER: US/10/374,780A  
CURRENT FILING DATE: 2003-02-25  
PRIOR APPLICATION NUMBER: 09/837,944  
PRIOR FILING DATE: 2001-04-18  
PRIOR APPLICATION NUMBER: 60/310,847  
PRIOR FILING DATE: 2001-08-09  
PRIOR APPLICATION NUMBER: 09/934,455  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: 60/336,049  
PRIOR FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/338,692  
PRIOR FILING DATE: 2001-12-11  
PRIOR APPLICATION NUMBER: 10/171,468  
PRIOR FILING DATE: 2002-06-14  
PRIOR APPLICATION NUMBER: 10/225,066  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: 09/837,444  
PRIOR FILING DATE: 2002-08-09

```

; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 362
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: G1902 (conserved domain in AA coordinates:31-59)
US-10-374-780A-362

```

```

Query Match      27.7%; Score 377.5; DB 15; Length 204;
Best Local Similarity 48.8%; Pred. No. 1.5e-26;
Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;

```

```

Qy 26 QOQLPCPCDSSNTKFCYNNYNNFSGPRHFCACRRYTHGGTLRDVPVGGGTRKSAKR 85
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 EOQLKPCRCDSPTKFCYNNYNNLSQPRHFCSCRRYTHGGTLRVNVPVGGGSRKNATK 84
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 86 SRTCSNSSSSVSGVNSNGVPLQTPVLFPOSISNGVTHT-----VTESDGKSA 138
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 RSTSSSSASSPSN--SQNKKTKNPDPPDRNSQKPDLDPTRMLYGFFIGDDVVG-- 140
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 139 LSLGCSFTSTLLNHNMAATATHGSGSVTIGGFGIGL-GSGFDDVSFGLG 187
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 141 MEIGGSFSSLANN-----MQLGGGGIMLDGSGMDHPGMGLG 179
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 11
US-10-225-066A-406
; Sequence 406, Application US/10225066A
; Publication No. US20050160493A9
; GENERAL INFORMATION:
; APPLICANT: Mendel Biotechnology, Inc.
; APPLICANT: RATCLIFFE, Oliver
; APPLICANT: RIECHMANN, Jose Luis
; APPLICANT: ADAM, Luc J
; APPLICANT: DUBELL, Arnold T
; APPLICANT: HEARD, Jacqueline E
; APPLICANT: PILGRIM, Marsha L
; APPLICANT: JIANG, Cai-Zhong
; APPLICANT: REUBER, T. Lynne
; APPLICANT: CREELMAN, Robert A
; APPLICANT: PINEDA, Omalra
; APPLICANT: YU, Guo-Liang
; APPLICANT: BROUN, Pierre E
; TITLE OF INVENTION: Yield-Related Polynucleotides and Polypeptides in Plants
; FILE REFERENCE: MEI0036-2 US
; CURRENT APPLICATION NUMBER: US/10/225,066A
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 09/837,444
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 1122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 406
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-225-066A-406

```

```

Query Match      27.7%; Score 377.5; DB 18; Length 204;
Best Local Similarity 48.8%; Pred. No. 1.5e-26;
Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;

```

```

Qy 26 QOQLPCPCDSSNTKFCYNNYNNFSGPRHFCACRRYTHGGTLRDVPVGGGTRKSAKR 85
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 EOQLKPCRCDSPTKFCYNNYNNLSQPRHFCSCRRYTHGGTLRVNVPVGGGSRKNATK 84
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 86 SRTCSNSSSSVSGVNSNGVPLQTPVLFPOSISNGVTHT-----VTESDGKSA 138
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 RSTSSSSASSPSN--SQNKKTKNPDPPDRNSQKPDLDPTRMLYGFFIGDDVVG-- 140
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 139 LSLGCSFTSTLLNHNMAATATHGSGSVTIGGFGIGL-GSGFDDVSFGLG 187
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 141 MEIGGSFSSLANN-----MQLGGGGIMLDGSGMDHPGMGLG 179
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 12
US-10-425-114-40748
; Sequence 40748, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 40748
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB25-078-G1_FLI.pep
US-10-425-114-40748

```

```

Query Match      27.7%; Score 377.5; DB 15; Length 206;
Best Local Similarity 48.8%; Pred. No. 1.5e-26;
Matches 83; Conservative 21; Mismatches 43; Indels 23; Gaps 5;

```

```

Qy 26 QOQLPCPCDSSNTKFCYNNYNNFSGPRHFCACRRYTHGGTLRVNVPVGGGTRKSAKR 85
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 EOQLKPCRCDSPTKFCYNNYNNLSQPRHFCSCRRYTHGGTLRVNVPVGGGSRKNATK 86
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 86 SRTCSNSSSSVSGVNSNGVPLQTPVLFPOSISNGVTHT-----VTESDGKSA 138
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 87 RSTSSSSASSPSN--SQNKKTKNPDPPDRNSQKPDLDPTRMLYGFFIGDDVVG-- 142
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 139 LSLGCSFTSTLLNHNMAATATHGSGSVTIGGFGIGL-GSGFDDVSFGLG 187
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 143 MEIGGSFSSLANN-----MQLGGGGIMLDGSGMDHPGMGLG 181
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 13
US-10-424-599-187121
; Sequence 187121, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 187121
; LENGTH: 211
; TYPE: PRT
US-10-424-599-187121

```

```

: ORGANISM: Glycine max
:
: FEATURE:
:
: OTHER INFORMATION: Clone ID: PAT_MRT3847_139983C.1.pep
US-10-424-599-187121

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Query Match	27.6%;	Score 376.5;	DB 15;	Length 211;
Best Local Similarity	39.8%;	Pred. No. 1.9e-26;		
Matches 96;	Conservative 25;	Mismatches 77;	Indels 43;	Gaps 8

Qy	18	GVAVPISLDDQEQQLPCPCRCSSNTWKFCYNNYNNFSPRHFCAACRYYMTHTGLDVPVG	77
Qy	9	GVAPQPEPEQEQKPCRCDSNMTKFCYNNYNNLSQPRHFCNCRYYMTKGGALFNIIYVG	68
Qy	78	GTRKSAKRRT--CNSSSSVSGVVSNSGVPLDTTVLFPQSSISNGVTHVTBSGK	135
Db	69	GSARKTKRSSSTLSSKRSSAPSSSSAVSDPDPRICTNFPDODORVLNG-----	117
Qy	136	GSALSLCGSPFTSTLNLHNAATAATNG---SGSVIGIGGFGIGLGSFPDDVFGIGRAMWP	192
Db	118	-----GGSPFSLIASGGHFTLLBGLNPSGGGLNKGFEVGVSS--DPLGALDGLNP	168
Qy	193	FSTVGTATTNNVSGNGHAAVMPAPATWQFEGLESNAGGFPVSGEYFAWPDLSITTPGNSL	252
Db	169	-----DIAQVQSNSENS-----FLGIQ--NGDSSCNGNTH--GMSDLAITTPGPSPF	210
Qy	253	K 253	
Db	211	Q 211	

RESULT 14  
US-10-425-114-43084

```

GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E.
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(5313)B
CURRENT FILING DATE: 2003-04-26
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 43084
LENGTH: 211
TYPE: PRT
ORGANISM: Glycine max
FEATURES:
OTHER INFORMATION: Clone ID: 700685541_FLT.pep
IS-10-425-114-43084

```

Query Match	27.6%;	Score 376.5;	DB 15;	Length 211;
Best Local Similarity	39.8%;	Pred. No. 1,9e-26;		
Matches 96;	Conservative 25;	Mismatches 77;	Indels 43;	Gaps 8

QY 18 GTVVPISLDOEOLPCPCRSSNTKCYNNVNFSPRFECACGRYTHGGTLEADVGG 77  
 Db 9 GVAPEPPEDOLKCRCDNNTKFCYNNYNTLSPPRFECNCKRYTNGKALNINIVGG 68  
 QY 78 GTRKAKAKRGT--CSNSSSSVSGVNSNGVPLOTTVPYLEPSSISNGYTHVTESDGK 135  
 Db 69 GSAKITTKRSSSTLSKRSASPPSSASVSDPDPRTICNTVDODQVNLG----- 117  
 QY 136 GSAISLCSGFFSTFLNHNAAATATG---SGSVIGIGFGIGLCSGFDVSGFLGRAMWP 192  
 Db 118 -----GGSFSLIASGCHFTLLBGLNPPSSGGLKMGSEFVGVSS---DPLNIDSLNP 168  
 QY 193 FSTVGTATTNTTNGSNGHHAVMPALTWQFEGLESNAGGFVSGEYFAMPDLSTTPGNLSL 252

Dd 169 -----DLQVQSNENSES-----FLGLQ-NGDSCWNGTH-GMSDLATTPGSPF 210  
QY 253 K 253  
Db 211 Q 211

```

RESULT 15
US-10-424-599-239234
, Sequence 239234, Application US/10424599
, Publication No. US20040031072A1
, GENERAL INFORMATION:
, APPLICANT: La Rosa Thomas J
, APPLICANT: Kovalic David K
, APPLICANT: Zhou Yihua
, APPLICANT: Cao Yongwei
, TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
, TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
, FILE REFERENCE: 38-21(53223)B
, CURRENT APPLICATION NUMBER: US/10/424,599
, NUMBER FILING DATE: 2003-04-28
, NUMBER OF SEQ ID NOS: 285684
, SEQ ID NO 239234
, LENGTH: 211
, TYPE: PRT
, ORGANISM: Glycine max
, FEATURES:
, OTHER INFORMATION: Clone ID: PAT_MRT3847_58053C.1.pep
, US-10-424-599-239234

```

Query Match	26.1%;	Score 356;	DB 15;	Length 211;
Best Local Similarity	36.4%;	Pred. No. 1.5e-24;		
Matches	92;	Conservative 28;	Mismatches 65;	Indels 68; Gaps 10

[illegible]

Search completed: November 3, 2005, 16:17:25  
Job time : 168 secs

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